

10.805 - 281

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:38:05 ; Search time 23.5 Seconds  
(without alignments)  
20.472 Million cell updates/sec

Title: SEQ1  
Perfect score: 27  
Sequence: 1 ffglm 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	66.7	5	2 PT0278	Ig heavy chain CRD
2	14	51.9	5	2 A44955	alkanal monooxygen
3	12	44.4	4	2 JQ1273	neuropeptide Antho
4	11	40.7	5	2 A61445	Met-enkephalin - b
5	10	37.0	4	2 PT0240	Ig heavy chain CRD
6	10	37.0	4	2 A53284	T-cell receptor be
7	10	37.0	5	2 G44817	27.5 kda structura
8	10	37.0	5	2 I44817	27.5K structural p
9	10	37.0	5	2 E44817	27.5K structural p
10	10	37.0	5	2 C44817	28.5K structural p
11	10	37.0	5	2 A44817	28K structural pro
12	9	33.3	3	3 S68328	blood cell protein
13	9	33.3	5	2 A32516	cholecystokinin-5
14	9	33.3	5	2 PQ0689	photosystem I 10.4
15	9	33.3	5	2 B61445	Leu-enkephalin - b
16	8	29.6	4	2 PT0633	T-cell receptor be
17	8	29.6	5	2 PT0572	T-cell receptor be
18	7	25.9	4	3 B23751	spinal cord peptid
19	7	25.9	4	2 E44823	synaptosomal-assoc
20	7	25.9	4	2 B53284	T-cell receptor be
21	7	25.9	5	2 T10954	hypothetical prote
22	7	25.9	5	2 JH0253	gut pentapeptide -
23	7	25.9	5	2 S69237	surface protein te
24	6	22.2	3	3 PT0636	T-cell receptor be
25	6	22.2	3	3 PT0571	T-cell receptor be
26	6	22.2	3	3 GKHU	growth-modulating
27	6	22.2	3	3 A60898	bursin - chicken
28	6	22.2	3	3 A23751	spinal cord peptid
29	6	22.2	4	1 ECXAA	antho-RFamide neur

30	6	22.2	4	2 D41654	hypothetical prote
31	6	22.2	4	2 S53508	starvation-induced
32	6	22.2	4	2 T30569	hypothetical prote
33	6	22.2	4	2 I38888	COI intron 16 prot
34	6	22.2	4	2 A25844	autho-RF amide neu
35	6	22.2	4	2 A34626	RPCN-related neuro
36	6	22.2	4	2 S39390	myosin-light-chain
37	6	22.2	4	2 S43959	Ig mu chain V regi
38	6	22.2	4	2 S47552	ubiquitin - rat
39	6	22.2	4	2 S09478	globulin IV alpha
40	6	22.2	4	2 PL0140	carbon-monoxide de
41	6	22.2	4	2 A35779	neuropeptide Antho
42	6	22.2	4	2 A60418	PMRFamide - polych
43	6	22.2	4	2 A32480	achatin-1 - giant
44	6	22.2	4	2 PT0271	Ig heavy chain CRD
45	6	22.2	4	2 PT0711	T-cell receptor be

ALIGNMENTS

RESULT 1

PT0278  
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0278  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A;Reference number: PT0222; MUID:91108337; PMID:1999102  
A;Accession: PT0278  
A;Molecule type: DNA  
A;Residues: 1-5 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 18; DB 2; Length 5;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5  
DB 1 YFGVL 5

RESULT 2

A4955  
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)  
C;Species: Vibrio harveyi  
C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 26-May-2000  
C;Accession: A44955  
R;Paquette, O.; Tu, S.C.  
Photochem. Photobiol. 50, 817-825, 1989  
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib  
A;Reference number: A44955; MUID:90175700; PMID:2626493  
A;Accession: A44955  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <PAQ>  
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 51.9%; Score 14; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGL 4  
DB 1 FGI 3

RESULT 3

JQ1273

neuropeptide Antho-KAamide - sea anemone (Anthopleura elegantissima)  
 C:Species: Anthopleura elegantissima  
 C:Date: 31-Mar-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
 C:Accession: J01273  
 R:Norhacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.  
 Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991  
 A:Title: Isolation of L-3-phenylacetyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide  
 A:Reference number: J01273; PMID:92028852; PMID:1681803  
 A:Accession: J01273  
 A:Molecule type: protein  
 A:Residues: 1-4 <NOT>  
 A:Cross-references: UNIPROT:P58705  
 C:Comment: The carboxyl-terminal amide probably arises from cleavage of a following glycopeptide  
 C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation  
 F:1/Modified site: L-3-phenylacetic acid (Phe) #status experimental  
 F:4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FF 2  
 ||  
 Db 1 FF 2

RESULT 4  
 A61445  
 Met-enkephalin - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C:Accession: A61445  
 R:Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A:Reference number: A61445; PMID:8414823; PMID:6583690  
 A:Accession: A61445  
 A:Molecule type: protein  
 A:Residues: 1-5 <LEU>  
 A:Experimental source: pedal ganglia  
 C:Keywords: neuropeptide; opioid peptide

Query Match 40.7%; Score 11; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GLM 5  
 ||  
 Db 3 GFM 5

RESULT 5  
 PT0240  
 Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0240  
 R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; PMID:91108337; PMID:1899102  
 A:Accession: PT0240  
 A:Molecule type: DNA  
 A:Residues: 1-4 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 37.0%; Score 10; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
 ||  
 Db 3 GL 4

neuropeptide Antho-KAamide - sea anemone (Anthopleura elegantissima)  
 C:Species: Anthopleura elegantissima  
 C:Date: 31-Mar-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
 C:Accession: J01273  
 R:Norhacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.  
 Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991  
 A:Title: Isolation of L-3-phenylacetyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide  
 A:Reference number: J01273; PMID:92028852; PMID:1681803  
 A:Accession: J01273  
 A:Molecule type: protein  
 A:Residues: 1-4 <NOT>  
 A:Cross-references: UNIPROT:P58705  
 C:Comment: The carboxyl-terminal amide probably arises from cleavage of a following glycopeptide  
 C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation  
 F:1/Modified site: L-3-phenylacetic acid (Phe) #status experimental  
 F:4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FF 2  
 ||  
 Db 1 FF 2

RESULT 4  
 A61445  
 Met-enkephalin - blue mussel  
 C:Species: Mytilus edulis (blue mussel)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C:Accession: A61445  
 R:Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A:Reference number: A61445; PMID:8414823; PMID:6583690  
 A:Accession: A61445  
 A:Molecule type: protein  
 A:Residues: 1-5 <LEU>  
 A:Experimental source: pedal ganglia  
 C:Keywords: neuropeptide; opioid peptide

Query Match 40.7%; Score 11; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GLM 5  
 ||  
 Db 3 GFM 5

RESULT 5  
 PT0240  
 Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0240  
 R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; PMID:91108337; PMID:1899102  
 A:Accession: PT0240  
 A:Molecule type: DNA  
 A:Residues: 1-4 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 37.0%; Score 10; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
 ||  
 Db 3 GL 4

Db 3 GL 4

RESULT 6  
 A53284  
 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C:Accession: A53284  
 R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
 Mol. Immunol. 28, 881-888, 1991  
 A:Title: Evolutionarily conserved organization and sequences of germline diversity and J  
 A:Reference number: A53284; PMID:91342695; PMID:1678859  
 A:Accession: A53284  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-4 <HAR>  
 A:Cross-references: GB:S60737; NID:9233916; PIDN:AAB19517.1; PID:9233917  
 A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)  
 C:Keywords: T-cell receptor

Query Match 37.0%; Score 10; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
 ||  
 Db 1 GL 2

RESULT 7  
 G44817  
 27.5 kda structural protein - Leuconostoc oenos phage P32 (fragment)  
 C:Species: Leuconostoc oenos phage P32  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: G44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos  
 A:Reference number: A44817; PMID:92085033; PMID:1748868  
 A:Accession: G44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 37.0%; Score 10; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
 ||  
 Db 4 GL 5

RESULT 8  
 I44817  
 27.5K structural protein - Leuconostoc oenos phage P37 (fragment)  
 C:Species: Leuconostoc oenos phage P37  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: I44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos  
 A:Reference number: A44817; PMID:92085033; PMID:1748868  
 A:Accession: I44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 37.0%; Score 10; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
 ||  
 Db 4 GL 5

Query Match 37.0%; Score 10; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
 ||  
 Db 4 GL 5

QY 3 GL 4  
||  
Db 4 GL 5

## RESULT 9

E44817  
27.5K structural protein - Leuconostoc oenos phase P54 (fragment)  
C/Species: Leuconostoc oenos phase P54  
C/Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C/Accession: E44817  
R/Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A/Title: Lysogeny in Leuconostoc oenos.  
A/Reference number: A44817; MUID:92085033; PMID:1748868  
A/Molecule type: protein  
A/Residues: 1-5 <ARB>  
A/Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 37.0%; Score 10; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4  
||  
Db 4 GL 5

## RESULT 10

C44817  
28.5K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)  
C/Species: Leuconostoc oenos phase PAT5-12  
C/Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C/Accession: C44817  
R/Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A/Title: Lysogeny in Leuconostoc oenos.  
A/Reference number: A44817; MUID:92085033; PMID:1748868  
A/Accession: C44817  
A/Molecule type: protein  
A/Residues: 1-5 <ARB>  
A/Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 37.0%; Score 10; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4  
||  
Db 4 GL 5

## RESULT 11

A44817  
28K structural protein - Leuconostoc oenos phase PZt11-15 (fragment)  
C/Species: Leuconostoc oenos phase PZt11-15  
C/Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C/Accession: A44817  
R/Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A/Title: Lysogeny in Leuconostoc oenos.  
A/Reference number: A44817; MUID:92085033; PMID:1748868  
A/Accession: A44817  
A/Molecule type: protein  
A/Residues: 1-5 <ARB>  
A/Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 37.0%; Score 10; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4

Db ||  
4 GL 5

## RESULT 12

S68328  
blood cell protein A - Molgula manhattensis (fragment)  
C/Species: Molgula manhattensis  
C/Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C/Accession: S68328  
R/Taylor, S.W.; Ross, M.M.; Waite, J.H.  
Arch. Biochem. Biophys. 324, 228-240, 1995  
A/Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from t1  
A/Reference number: S68325; MUID:96132650; PMID:8554314  
A/Accession: S68328  
A/Molecule type: protein  
A/Residues: 1-3 <TAV>

Query Match 33.3%; Score 9; DB 3; Length 3;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2  
|:  
Db 2 FY 3

## RESULT 13

A32516  
cholecystokinin-5 - dog  
N/Alternate names: CCK-5  
C/Species: Canis lupus familiaris (dog)  
C/Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C/Accession: A32516  
R/Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.  
Am. J. Physiol. 252, G272-G275, 1987  
A/Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest  
A/Reference number: A32516; MUID:87153871; PMID:3826354  
A/Accession: A32516  
A/Molecule type: protein  
A/Residues: 1-5 <SHI>  
C/Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystat  
C/Superfamily: gastrin  
C/Keywords: amidated carboxyl end; neuropeptide  
F/5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 33.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GLM 5  
||  
Db 1 GWM 3

## RESULT 14

PQ0689  
photosystem I 10.4K H1 chain - common tobacco (fragment)  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C/Accession: PQ0689  
R/Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.  
Plant Physiol. 102, 1259-1267, 1993  
A/Title: Molecular heterogeneity of photosystem I. psalD, psalF, psalH and psal are  
A/Reference number: PQ0667; MUID:94105345; PMID:8278548  
A/Accession: PQ0689  
A/Molecule type: protein  
A/Residues: 1-5 <OEO>  
C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 33.3%; Score 9; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Wed Mar 23 15:33:42 2005

```

QY      2 FG 3
      :|
Db      2 YG 3

RESULT 15
B61445
Leu-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: B61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A:Reference number: A61445; MUID:84144823; PMID:6583690
A:Accession: B61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match      33.3%; Score 9; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FG 3
      :|
Db      1 YG 2

Search completed: March 23, 2005, 14:51:53
Job time : 25.5 secs

```



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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:21:29 ; Search time 112.5 Seconds  
(without alignments)  
22.759 Million cell updates/sec

Title: SEQ1  
Perfect score: 27  
Sequence: 1 ffglm 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 53

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	59.3	5	1	AL14_CARMA	P81817 carcinus ma
2	12	44.4	4	1	FFKA_ATEL	P58705 anthopleura
3	12	44.4	4	1	OCPI_OCTMI	P38648 octopus min
4	12	44.4	5	1	PAP2_PARMA	P81864 pardachirus
5	12	44.4	5	1	RE11_LITRU	P82070 litoria rub
6	12	44.4	5	1	RE21_LITRU	P82071 litoria rub
7	12	44.4	5	1	RE31_LITRU	P82072 litoria rub
8	12	44.4	5	1	RE32_LITRU	P82073 litoria rub
9	12	44.4	5	1	UC22_MAIZE	P80628 zea mays (m
10	11	40.7	5	1	TPIS_CANFA	P54714 canis famil
11	9	33.3	4	1	FYRI_ATEL	P58706 anthopleura
12	9	33.3	4	1	ILME_SEPOP	P83568 sepia offic
13	7	25.9	5	1	UF01_MOUSE	P38639 mus musculu
14	6	22.2	2	1	GWA_SEPOP	P83570 sepia offic
15	6	22.2	3	1	GRWM_HUMAN	P01157 homo sapien
16	6	22.2	4	1	ACH1_ACHFU	P35904 achatina fu
17	6	22.2	4	1	DCML_PSECH	P19916 pseudomonas
18	6	22.2	4	1	EOSI_HUMAN	P02731 homo sapien
19	6	22.2	4	1	FAR3_HIRME	P42562 hirudo medi
20	6	22.2	4	1	FAR4_HIRME	P42563 hirudo medi
21	6	22.2	4	1	FLRF_HIRME	P42561 hirudo medi
22	6	22.2	4	1	FLRN_ATEL	P58707 anthopleura
23	6	22.2	4	1	FMRF_MAGNI	P01162 macrocallis
24	6	22.2	4	1	OCPI_OCTMI	P58649 octopus min
25	6	22.2	4	2	Q16047	Q16047 homo sapien
26	6	22.2	5	1	AP21_EISFO	P84182 eisenia foe
27	6	22.2	5	1	EI03_LITRU	P82099 litoria rub
28	6	22.2	5	1	EI04_LITRU	P82100 litoria rub
29	6	22.2	5	1	FARP_ARTTR	P41853 artiopeothi
30	6	22.2	5	1	FARP_CHICK	P83308 gallus gall
31	6	22.2	5	1	SUGA_ACHDO	P19991 acheta dome

32 6 22.2 5 1 UXAA\_CHLTR P38005 chlamydia t  
33 5 18.5 4 1 DCMS\_PSECH P3918 pseudomonas  
34 5 18.5 4 2 Q96AT0 Q96at0 homo sapien  
35 5 18.5 5 1 BIOA\_CITFR P13071 citrobacter  
36 5 18.5 5 1 BIOB\_CITFR P12997 citrobacter  
37 5 18.5 5 2 Q99007 Q99007 hordeum vul  
38 5 18.5 5 2 P83073 P83073 bacillus ce  
39 4 14.8 4 2 Q08433 Q08433 rattus sp.  
40 4 14.8 5 1 PRCT\_CARMA P67857 carcinus ma  
41 4 14.8 5 1 PRCT\_LIMPO P67858 limulus pol  
42 4 14.8 5 1 PRCT\_PERAM P67859 periplaneta  
43 3 11.1 5 1 PSK\_DAUCA P58261 daucus caro  
44 2 7.4 3 1 LUXE\_VIRFI P24272 vibrio fisc  
45 1 3.7 4 1 YLM\_YEAST P36515 saccharomyc

## ALIGNMENTS

RESULT 1  
AL14\_CARMA STANDARD; PRT; 5 AA.  
ID AL14\_CARMA  
AC P81817;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Carcinustatin 14.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.  
CC -!- SIMILARITY: Belongs to the allatostatin family.  
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.  
FT MOD\_RES 5 5 Leucine amide (Potential).  
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB30000 CRC64;  
Query Match 59.3%; Score 16; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 FGL 4  
Db 3 FGL 5

RESULT 2  
FFKA\_ATEL STANDARD; PRT; 4 AA.  
ID FFKA\_ATEL  
AC P58705;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antho-KAamide.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynantheseae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RC MEDLINE=92028852; PubMed=1681803;  
RX Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;  
RA "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a

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RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211 (1991).
RN [2]
RP FUNCTION
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Notherker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Ramide."
RL Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188 (1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC PIR: J01273; J01273.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 1 1 3-phenyllactic acid.
FT MOD RES 4 1 Alanine amide.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels -0; Gaps 0;

QY 1 FF 2
DB 1 FF 2

RESULT 3
OCPI OCTMI STANDARD; PRT; 4 AA.
AC P58628;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor."
RL Peptides 21:623-630 (2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less active
CC than Ocp-1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE-Ref.1.
KW D-amino acid; Direct protein sequencing; Hormone.
FT MOD RES 2 2
FT MOD RES 4 2
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FG 3
DB 2 FG 3

RESULT 4
PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidi; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE
RX TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus)."
RL J. Biol. Chem. 261:16704-16713 (1986).
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels in
CC membranes. At high concentration causes cell membrane lysis.
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pardaxin family.
KW Direct protein sequencing; Toxin.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2
DB 2 FF 3

RESULT 5
RE11 LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963 (1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=598; METHOD=PAB; RANGE=1-5; NOTE-Ref.1.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9C82A000000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2
DB 1 FF 3

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Db 3 FF 4

Query Match 44.4%; Score 12; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

RE21 LITRU  
ID RE21 LITRU STANDARD; PRT; 5 AA.  
AC P82071;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Rubellidin 2.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
'Litoria rubella'. The skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.  
KW Amphibian defense peptide; Direct protein sequencing.  
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FF 2  
Db 3 FF 4

RESULT 7

RE31 LITRU  
ID RE31 LITRU STANDARD; PRT; 5 AA.  
AC P82072;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Rubellidin 3.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
'Litoria rubella'. The skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.  
KW Amphibian defense peptide; Direct protein sequencing.  
FT MOD RES 5  
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FF 2  
Db 3 FF 4

RESULT 8

RE32 LITRU  
ID RE32 LITRU STANDARD; PRT; 5 AA.  
AC P82073;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Rubellidin 3.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria rubella".  
RL Aust. J. Chem. 52:639-645(1999).  
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
KW Amphibian defense peptide; Direct protein sequencing.  
SQ SEQUENCE 5 AA; 570 MW; 71A9C9CB2A000000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FF 2  
Db 3 FF 4

RESULT 9

UC22 MAIZE  
ID UC22 MAIZE STANDARD; PRT; 5 AA.  
AC P80628;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 474)  
(fragment).  
DE (fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Tounet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -1- MISCCELLANEOUS: On the 2D-gel the determined pI of this unknown  
protein is: 6.1, its MW is: 30.4 kDa.  
DR Maize-2DPAGE; P80628; COLSOPTILE.  
DR MaizeDB; 123954; --  
KW Direct protein sequencing.

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FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2
DB 2 FF 3

RESULT 10
TPIS CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate
isomerase) (Fragment).
GN Name=TPIS;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
phosphate.
CC -1- PATHWAY: Plays an important role in several metabolic pathways.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro; IPR000652; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
DR Direct protein sequencing; Fatty acid biosynthesis; Gluconeogenesis;
KW Glycolysis; Isomerase; Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 40.7%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFG 3
DB 1 FVG 3

RESULT 11
FYRI-ANTEL STANDARD; PRT; 4 AA.
AC P58706;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Anthopleura.
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-2;

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RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-
RT phenyllactyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Riamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT CHAIN 1 4 Antho-Riamide I.
FT CHAIN 2 4 Antho-Riamide II.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Isoleucine amide.
FT SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 33.3%; Score 9; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FF 2
DB 1 FY 2

RESULT 12
ILME-SEPOF STANDARD; PRT; 4 AA.
AC P83568;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pheromone peptide ILME.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Egg;
RX MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis.";
RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
RN [2]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -1- FUNCTION: Has myotropic activity targeting the genital tract.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg (SC2).
CC -1- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 33.3%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 LM 5  
Db 2 LM 3

RESULT 13  
UF01\_MOUSE  
ID UF01\_MOUSE STANDARD; PRT; 5 AA.  
AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins using  
RT preparative two-dimensional gel electrophoresis."  
RL Electrophoresis 15:735-745(1994).  
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 6.6, its MW is: 19 kDa.  
KW Direct protein sequencing.  
FT NON TER 5  
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 25.9%; Score 7; DB 1; Length 5;  
Best Local Similarity 33.3%; Pred. No. 1.6e+06;  
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PFG 3  
Db 1 WIG 3

RESULT 14  
GWA\_SEPOF  
ID GWA\_SEPOF STANDARD; PRT; 2 AA.  
AC P83570;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide Gwa.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
RT peptide inhibiting the motility of the mature oviduct in the  
RT cuttlefish, Sepia officinalis."  
RL Peptides 18:1469-1474(1997).  
CC -1- FUNCTION: Regulatory neuropeptide with myotropic activity  
CC targeting the distal oviduct. Inhibits the motility of the oviduct  
CC by decreasing tonus, frequency and amplitude of contractions.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 2  
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
Db 1 G 1

RESULT 15  
GRWM\_HUMAN  
ID GRWM\_HUMAN STANDARD; PRT; 3 AA.  
AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Growth-modulating peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77162369; PubMed=858356;  
RA Schlesinger D.H., Pickart L., Thaler M.M.;  
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine."  
RL Experientia 33:324-325(1977).  
CC -1- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
CC growth of some cell types and to inhibit other types in vitro.  
DR GO; GO:0001558; P:regulation of cell growth; NAS.  
KW Direct protein sequencing.  
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 22.2%; Score 6; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3  
Db 1 G 1

Search completed: March 23, 2005, 14:49:56  
Job time : 117.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 15:19:16 ; Search time 68 Seconds  
(without alignments)  
28.438 Million cell updates/sec

Title: SRQ1

Perfect score: 27

Sequence: 1 ffglm 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 45841

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A\_Geneseq\_16Dec04:\*
- 2: Geneseqp1980s:\*
- 3: Geneseqp1990s:\*
- 4: Geneseqp2000s:\*
- 5: Geneseqp2001s:\*
- 6: Geneseqp2002s:\*
- 7: Geneseqp2003as:\*
- 8: Geneseqp2003bs:\*
- 9: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	2 AAR33009	Aar33009 Alpha-sub
2	27	100.0	5	2 AAR33008	Aar33008 Alpha-sub
3	27	100.0	5	2 AAR33007	Aar33007 Alpha-sub
4	27	100.0	5	2 AAR33010	Aar33010 Alpha-sub
5	27	100.0	5	2 AAR54549	Aar54549 Cholecyst
6	27	100.0	5	2 AAR54551	Aar54551 Cholecyst
7	27	100.0	5	2 AAR54550	Aar54550 Cholecyst
8	27	100.0	5	2 AAR54548	Aar54548 Cholecyst
9	27	100.0	5	2 AAW11687	Aaw11687 Tetrapt
10	27	100.0	5	2 AAW99643	Aaw99643 Substance
11	27	100.0	5	2 AAY50325	Aay50325 Neutroph
12	27	100.0	5	2 AAW92660	Aaw92660 Human tac
13	27	100.0	5	3 AAB23025	Aab23025 Human/rat
14	27	100.0	5	3 AAY67576	Aay67576 P antag
15	27	100.0	5	4 AAB91428	Aab91428 Tachykini
16	27	100.0	5	5 ABB10088	Abb10088 Substance
17	27	100.0	5	5 AAW77845	Aaw77845 Tachykini
18	27	100.0	5	7 ADE94203	Ade94203 High acti
19	27	100.0	5	7 ADF92530	Adf92530 Substance
20	27	100.0	5	8 ADM95078	Adm95078 Mammalian
21	27	100.0	5	8 ADR43771	Adr43771 Human mag
22	24	88.9	5	2 AAW92702	Aaw92702 Human tac
23	24	88.9	5	5 ABB10089	Abb10089 Substance
24	24	88.9	5	7 ADE94204	Ade94204 High acti
25	22	81.5	5	2 AAR27697	Aar27697 Cyclic ta

26	22	81.5	5	2 AAW92703	Aaw92703 Human tac
27	22	81.5	5	2 AAW92701	Aaw92701 Human tac
28	21	77.8	4	2 AAW41683	Aaw41683 Peptide u
29	21	77.8	4	2 AAY31075	Aay31075 Non-cross
30	21	77.8	4	3 AAB23026	Aab23026 Human/rat
31	21	77.8	4	3 AAY67577	Aay67577 P antag
32	21	77.8	4	4 AAB91447	Aab91447 Tachykini
33	21	77.8	4	5 ABB10091	Abb10091 Substance
34	21	77.8	4	5 AAU77846	Aau77846 Tachykini
35	21	77.8	4	7 ADE94198	Ade94198 High acti
36	21	77.8	4	8 ADR43772	Adr43772 Human mag
37	21	77.8	5	4 AAB91389	Aab91389 Tachykini
38	21	77.8	5	5 ABB10090	Abb10090 Substance
39	21	77.8	5	6 AAE35975	Aae35975 Zea mays
40	21	77.8	5	7 ADE94205	Ade94205 High acti
41	21	77.8	5	8 ADR03603	Adr03603 E. coli m
42	20	74.1	5	2 AAW80134	Aaw80134 COOH-term
43	20	74.1	5	2 AAR41695	Aar41695 GHRP-6 (G
44	20	74.1	5	2 AAR47524	Aar47524 GHRP-6 an
45	20	74.1	5	2 AAW13221	Aaw13221 Growth ho

#### ALIGNMENTS

##### RESULT 1

AAR33009

ID AAR33009 standard; peptide; 5 AA.

XX AAR33009;

AC AAR33009;

XX AAR33009;

DT 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

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XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

XX AAR33009;

CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX Sequence 5 AA;  
 SQ

Query Match 100.0%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5  
 DB 1 FFGLM 5

RESULT 2  
 AAR33008  
 ID AAR33008 standard; peptide; 5 AA.

XX AAR33008;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-APR-1993 (first entry)  
 XX  
 DE Alpha-substituted short peptide.  
 XX  
 CC; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
 KW improved bioavailability.  
 XX Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 2 /note= "alpha-Me-Phe"  
 FT Modified-site 5 /note= "Met-NH2"  
 FT

XX WO9219254-A1.  
 XX 12-NOV-1992.  
 XX 15-APR-1992; 92WO-US003119.  
 XX 24-APR-1991; 91US-00690755.  
 XX 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.

XX Horwell DC, Hughes J, Richardson RS, Howson W;  
 XX WPI; 1992-398522/48.

XX New alpha-substd. polypeptide are e.g. selective receptor ligands - for  
 FT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
 PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
 CC substituent on an alpha-C atom in the chain. Such substitution may modify  
 CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,

CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX Sequence 5 AA;

SQ

Query Match 100.0%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5  
 DB 1 FFGLM 5

RESULT 3  
 AAR33007  
 ID AAR33007 standard; peptide; 5 AA.

XX AAR33007;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-APR-1993 (first entry)  
 XX  
 DE Alpha-substituted short peptide.  
 XX  
 CC; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
 KW improved bioavailability.  
 XX Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "alpha-Me-Phe"  
 FT Modified-site 5 /note= "Met-NH2"  
 FT

XX WO9219254-A1.  
 XX 12-NOV-1992.  
 XX 15-APR-1992; 92WO-US003119.  
 XX 24-APR-1991; 91US-00690755.  
 XX 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.

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 XX WPI; 1992-398522/48.

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 FT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
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 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
 CC substituent on an alpha-C atom in the chain. Such substitution may modify  
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 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR



CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5  
DB 1 FFGLM 5

RESULT 4  
AAR33010  
ID AAR33010 standard; peptide; 5 AA.

XX AAR33010;

XX 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
KW improved bioavailability.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 5 /note= "alpha-Me-Met-NH2"

XX WO9219254-A1.

XX 12-NOV-1992.

XX 15-APR-1992; 92WO-US003119.

XX 24-APR-1991; 91US-00690755.

PR 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.

XX Horwell DC, Hughes J, Richardson RS, Howson W;

XX WPI; 1992-398522/48.

XX New alpha-subst. polypeptide are e.g. selective receptor ligands - for  
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
CC substituent on an alpha-C atom in the chain. Such substitution may modify  
CC the bioavailability, stability or absorbability of the peptide and hence  
CC may improve the activity of the peptide as a drug. Depending on the  
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
CC peptide, etc.), the modified peptides are variously useful for treating  
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
CC addictive drug withdrawal symptoms, hypertension, heart failure,  
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
CC asthma, bladder dysfunction, psychosis and arthritis; and as  
CC contraceptives. (Updated on 25-MAR-2003 to correct PI field.) (Updated on  
CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5  
DB 1 FFGLM 5

RESULT 5

AAR54549  
ID AAR54549 standard; peptide; 5 AA.

XX AAR54549;

XX 25-MAR-2003 (revised)

DT 14-DEC-1994 (first entry)

XX Cholecystokinin analogue peptide #42.

XX Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;  
KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;  
KW heart failure; cognition; memory enhancement; spasticity; depression;  
KW diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.  
XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 2 /label= MePhe

FT Modified-site 5 /note= "Amidated C-terminal"

XX WO9409031-A1.

XX 28-APR-1994.

XX 14-OCT-1993; 93WO-US009809.

XX 19-OCT-1992; 92US-00963169.

PR 08-OCT-1993; 93US-00131693.

XX (WARN ) WARNER LAMBERT CO.

XX Horwell DC, Howson W, Hugues J, Richardson RS;

XX WPI; 1994-151243/18.

XX New cholecystokinin analogues - useful e.g. in treatment of pain,  
PT obesity, stroke, anxiety, and gastrointestinal ulcers.

XX Claim 3; Page 66; 73pp; English.

XX The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues  
CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,  
CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart  
CC failure, cognition, memory enhancement, spasticity, depression, diabetes,  
CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the  
CC treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5  
DB 1 FFGLM 5

RESULT 6

AAR54551  
ID AAR54551 standard; peptide; 5 AA.

```

XX AC AAR54551;
XX DT 25-MAR-2003 (revised)
XX DT 14-DEC-1994 (first entry)
XX DE Cholecystokinin analogue peptide #44.
XX KW Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
XX KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
XX KW heart failure; cognition; memory enhancement; spasticity; depression;
XX KW diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 5
XX FT Modified-site 5 /label= MeMet
XX FT /note= "Amidated C-terminal"
XX PN WO9409031-A1.
XX PD 28-APR-1994.
XX PF 14-OCT-1993; 93WO-US009809.
XX PR 19-OCT-1992; 92US-00963169.
XX PR 08-OCT-1993; 93US-00131693.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Horwell DC, Howson W, Hugues J, Richardson RS;
XX WPI; 1994-151243/18.
XX DR New cholecystokinin analogues - useful e.g. in treatment of pain,
XX PT obesity, stroke, anxiety, and gastrointestinal ulcers.
XX PS Claim 3; Page 66; 73pp; English.
XX CC The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
XX CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
XX CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
XX CC failure, cognition, memory enhancement, spasticity, depression, diabetes,
XX CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
XX CC treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 5 AA;
XX Query Match 100.0%; Score 27; DB 2; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 FFGLM 5
XX DB 1 FFGLM 5
XX RESULT 7
XX AAR54550
XX ID AAR54550 standard; peptide; 5 AA.
XX XX
XX AC AAR54550;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 14-DEC-1994 (first entry)
XX DE Cholecystokinin analogue peptide #43.
XX KW Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
XX KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
XX KW heart failure; cognition; memory enhancement; spasticity; depression;
XX KW

```

```

KW XX diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 3 /label= MeLeu
XX FT Modified-site 5
XX FT /note= "Amidated C-terminal"
XX PN WO9409031-A1.
XX PD 28-APR-1994.
XX PF 14-OCT-1993; 93WO-US009809.
XX PR 19-OCT-1992; 92US-00963169.
XX PR 08-OCT-1993; 93US-00131693.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Horwell DC, Howson W, Hugues J, Richardson RS;
XX WPI; 1994-151243/18.
XX DR New cholecystokinin analogues - useful e.g. in treatment of pain,
XX PT obesity, stroke, anxiety, and gastrointestinal ulcers.
XX PS Claim 3; Page 66; 73pp; English.
XX CC The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
XX CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
XX CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
XX CC failure, cognition, memory enhancement, spasticity, depression, diabetes,
XX CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
XX CC treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 5 AA;
XX Query Match 100.0%; Score 27; DB 2; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 FFGLM 5
XX DB 1 FFGLM 5
XX RESULT 8
XX AAR54548
XX ID AAR54548 standard; peptide; 5 AA.
XX XX
XX AC AAR54548;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 14-DEC-1994 (first entry)
XX DE Cholecystokinin analogue peptide #41.
XX KW Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
XX KW gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
XX KW heart failure; cognition; memory enhancement; spasticity; depression;
XX KW diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /label= Mephe
XX FT Modified-site 5
XX FT /note= "Amidated C-terminal"
XX FT
XX FT
XX FT

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PN W09409031-A1.  
 XX 28-APR-1994.  
 XX 14-OCT-1993; 93WO-US009809.  
 XX 19-OCT-1992; 92US-00963169.  
 PR 08-OCT-1993; 93US-00131693.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX Horwell DC, Howson W, Hugues J, Richardson RS;  
 XX WPI; 1994-151243/18.  
 XX New cholecystokinin analogues - useful e.g. in treatment of pain,  
 PT obesity, stroke, anxiety, and gastrointestinal ulcers.  
 XX Claim 3; Page 66; 73pp; English.  
 XX The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues  
 CC of cholecystokinin (CCK) which can be used to treat obesity, anxiety,  
 CC gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart  
 CC failure, cognition, memory enhancement, spasticity, depression, diabetes,  
 CC cancers, asthma, bladder dysfunction, psychosis, arthritis and in the  
 CC treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX.  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FFGLM 5  
 DB 1 FFGLM 5  
 RESULT 9  
 AAW41687  
 ID AAW41687 standard; peptide; 5 AA.  
 AC AAW41687;  
 XX 09-JUN-1998 (first entry)  
 DT Tetrapeptide #4.  
 XX Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;  
 KW keratitis; insulin like growth factor-I; IGF-I; eye drop.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 5 /note= "C-terminal amide"  
 FT W09749419-A1.  
 XX 31-DEC-1997.  
 XX 11-JUN-1997; 97WO-JP002015.  
 XX 26-JUN-1996; 96JP-00165612.  
 XX (SANT ) SANTEN PHARM CO LTD.  
 XX Nishida T, Nakamura M, Nakata K;  
 PI WPI; 1998-076907/07.  
 XX Ophthalmic drug composition containing tetra-peptide - is useful as

PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,  
 XX dry eye, keratitis.  
 XX Disclosure; Page 11; 19pp; Japanese.  
 XX This sequence is shown in the specification. The invention relates to an  
 CC ophthalmic drug composition which contains Phe-Gly-Leu-Met-NH2 or its  
 CC medicinally acceptable salts as the active ingredient. It is used,  
 CC together with insulin like growth factor-I (IGF-I), to treat corneal  
 CC disorders such as corneal ulcer, corneal epithelial peeling, dry eye and  
 CC keratitis. The dosage is 0.1-5000 (preferably 1-1000) mg/day of the  
 CC active ingredient and 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The  
 CC preferable form of the composition is eye drops  
 XX Sequence 5 AA;  
 SQ Query Match 100.0%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FFGLM 5  
 DB 1 FFGLM 5  
 RESULT 10  
 AAW99643  
 ID AAW99643 standard; peptide; 5 AA.  
 XX AAW99643;  
 AC AAW99643;  
 XX 21-MAY-1999 (first entry)  
 DT Substance P analogue peptide.  
 DE Substance P  
 XX Substace P; myoblast transfer therapy; pain relief; analgesic;  
 KW behavioural abnormality; perceptive abnormality; opioid receptor;  
 KW psychiatric condition; depression; chronic anxiety syndrome; paranoia;  
 KW alcoholism; drug addiction; chronic pain; neuron.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX EP898967-A1.  
 XX 03-MAR-1999.  
 XX 07-APR-1998; 98EP-00201068.  
 XX 11-AUG-1997; 97US-0055199P.  
 XX (CELL-) CELL THERAPY RES FOUND.  
 XX Law PK;  
 XX WPI; 1999-144555/13.  
 XX New composition for supplying peptide to opioid receptor - comprises  
 PT myogenic cells containing heterologous DNA encoding peptide and carrier.  
 XX Claim 8; Page 8; 11pp; English.  
 XX A composition has been developed for supplying a peptide to an opioid  
 CC receptor or that interferes with binding of substance P to its receptor.  
 CC The composition comprises: (a) myogenic cells that contain heterologous  
 CC DNA encoding the peptide to express the peptide; and (b) a  
 CC pharmaceutically acceptable carrier. The composition is useful for  
 CC relieving pain and for treating behavioural and perceptive abnormalities  
 CC using myoblast transfer therapy. It is useful in a method for treating  
 CC psychiatric conditions that involve abnormal perception e.g. depression,  
 CC chronic anxiety syndromes, paranoia, alcoholism and drug addiction,  
 CC chronic pain and other diseases in which opioid neurons and substance P  
 CC sensitive neurons play a role. The composition provides a continuous,

CC long term supply of opioid peptides (long-term analgesia) which lasts for  
 CC up to at least 6 years. The present sequence represents a specifically  
 CC claimed substance P analogue  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PFGLM 5  
 |||||  
 Db 1 PFGLM 5

## RESULT 11

AAV50325  
 ID AAV50325 standard; peptide; 5 AA.

XX  
 AC AAV50325;

XX 12-JAN-2000 (first entry)

XX Neutrophil-activating pancreatic derived peptide 125.

XX Cell activation; pancreas; treatment; cardiovascular disease; trauma;  
 XX inflammatory disease; autoimmune diseases; arthritis; diabetes; stroke;  
 KW organ rejection; ischemia; Alzheimer's disease; myocardial infarction;  
 KW haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina;  
 KW trauma; protease inhibitor; hypertension; sepsis.

XX Unidentified.

XX WO9946367-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-US005247.

XX 11-MAR-1998; 98US-00038894.

XX (CELL-) CELL ACTIVATION INC.

PA (REGC ) UNIV CALIFORNIA.

PA (SCRI ) SCRIPPS RES INST.

XX Stoughton RB, Schmid-Schonbein GW, Hugli TE, Kistler E;

XX WPI; 1999-580234/49.

XX Use of cell activating compositions in developing products for diagnosis  
 XX and treatment of e.g. cardiovascular, inflammatory, autoimmune or  
 PT Alzheimer's disease, trauma, arthritis, organ rejection, diabetes, stroke  
 PT or ischemia.

XX Example 9; Page 184; 184pp; English.

XX This invention describes a novel method for the use and preparation of  
 XX cell activating compositions which involves preparing a cell activating  
 XX composition comprising (a) homogenizing pancreatic tissue in buffer at  
 XX about neutral or higher pH to produce a homogenate; (b) removing  
 XX particulates from the homogenate; (c) optionally incubating the resulting  
 XX homogenate, with particulates removed, with a protease; and (d)  
 XX fractionating the homogenate and selecting fractions that exhibit cell  
 XX activation activity. The methods can be used for improving treatment  
 XX outcome or reducing risk of treatment of e.g. cardiovascular disease,  
 XX inflammatory disease, trauma, autoimmune diseases, arthritis, organ  
 XX rejection, diabetes and diabetic complications, stroke, ischemia,  
 XX Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic  
 XX retinopathy, diabetes, venous insufficiency, unstable angina or trauma.  
 XX They can be used in the veterinary treatment of a non-human subject.  
 XX Protease inhibitors can be used to lower cell activation resulting from  
 XX these diseases and deficiencies. The detection of an elevated level of  
 XX hydrogen peroxide can be used to detect an inflammatory condition. An

CC elevated level of hydrogen peroxide in plasma or whole blood and in the  
 CC presence of superoxide dismutase (SOD) indicates leukocyte up regulation,  
 CC e.g. indicative of the onset of an acute cardiovascular disorders, such  
 CC as disease onset or ischemic complications. An elevated level of hydrogen  
 CC peroxide in plasma or whole blood and a low level in the presence of SOD  
 CC is indicative of a chronic or immune compromised condition e.g.  
 CC hypertension or sepsis. AAV50201-Y50334 represent peptides used in the  
 CC method of the invention  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PFGLM 5  
 |||||  
 Db 1 PFGLM 5

## RESULT 12

AAW92660  
 ID AAW92660 standard; peptide; 5 AA.

XX  
 AC AAW92660;

XX 20-MAR-2003 (revised)

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #6.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;  
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;  
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX Homo sapiens.

XX US5876948-A.

XX 02-MAR-1999.

XX 29-JUL-1991; 91US-00737371.

XX 27-JUL-1990; 90US-00559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA;

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their  
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.

XX Disclosure; Col 13-14; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting  
 XX a neurotoxin. The method involves incubating tachykinin agonists with  
 XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be  
 XX used for identifying compounds for treating diseases characterised by an  
 XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,  
 XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage  
 XX with amyloidosis and non-inherited congophilic angiopathy with cerebral  
 XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human  
 XX beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF  
 XX field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 27; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 FFGLM 5
DB      1 FFGLM 5

RESULT 13
AAB23025
ID AAB23025 standard; peptide; 5 AA.
XX
AC AAB23025;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human/rat tachykinin Substance P C-terminal pentapeptide.
XX
KW Substance P; tachykinin; human; rat; magnesium binding defect;
KW sodium sensitive essential hypertension; insulin resistance;
KW type 2 diabetes; antibody; immunoassay; quantification.
XX
OS Homo sapiens.
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Modified-site 5 /note= "C-terminal amide"
FT FT
XX
PN WO200054053-A1.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US003707.
XX
PR 10-MAR-1999; 99US-00265690.
XX
PA (WELL/) WELLS I C.
XX
PI Wells IC;
XX
DR WPI; 2000-587457/55.
XX
PT Detecting magnesium binding defects associated with abnormal
PT physiological states such as sodium-sensitive essential hypertension and
PT type 2 insulin-resistant diabetes mellitus, comprises measuring a
PT specific pentapeptide in blood.
XX
PS Disclosure; Page 5; 21pp; English.
XX
CC The invention relates to a method for detecting magnesium binding
CC defects. The method comprises quantitating a tachykinin C-terminal
CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
CC AAB23026) in blood using an antibody specific for the generalised
CC mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-
CC NH2 (AAB23028). The method is useful for detecting cellular magnesium
CC binding defects which are associated with abnormal physiological states
CC such as sodium-sensitive essential hypertension and type 2 diabetes
CC mellitus. The present sequence represents the C-terminal 5 amino acids of
CC the tachykinin Substance P (AAB23027) from human and rat, which may be
CC assayed according to the method of the invention
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFGLM 5
DB      1 FFGLM 5

RESULT 14
AAY67576
ID AAY67576 standard; peptide; 5 AA.
XX
AC AAY67576;
XX
DT 19-MAY-2000 (first entry)
XX
DE P antagonist peptide #4.
XX
KW Pharmaceutical; veterinary; gonadotropin-releasing hormone; GnRH;
KW pore-forming agent; lecithin; stearin; P antagonist.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 5 /note= "C-terminal amide"
FT FT
XX
PN WO200004897-A1.
XX
PD 03-FEB-2000.
XX
PF 20-JUL-1999; 99WO-AU000585.
XX
PR 20-JUL-1998; 98AU-00004730.
PR 20-JUL-1998; 98AU-00004731.
PR 13-MAY-1999; 99AU-00000324.
XX
PA (PEPT-) PEPTTECH LTD.
XX
PI Trigg TE, Walsh JD, Rathjen DA;
XX
DR WPI; 2000-182528/16.
XX
PT Bioimplant formulation for sustained delivery of an active agent over 7
PT days to 2 years, comprises active agent, pore-forming agent and stearin.
XX
PS Claim 20; Page 21; 37pp; English.
XX
CC The invention provides a pharmaceutical and/or veterinary formulation
CC that comprises 2 -30% of active agents which include a gonadotropin-
CC releasing hormone (GnRH) agonist, 0.5 - 20% of a pore-forming agent which
CC is not lecithin, and the remainder stearin. The formulation is useful as
CC a sustained release implant which can deliver the active agent for a
CC period of 7 days to 2 years. Sequences AAY67573-578 represent P
CC antagonist peptides used in the composition
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFGLM 5
DB      1 FFGLM 5

RESULT 15
AAB91428
ID AAB91428 standard; peptide; 5 AA.
XX
AC AAB91428;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:604.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX

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PN WO200069900-A2.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000WO-US013576.  
 XX  
 PR 17-MAY-1999; 99US-0134406P.  
 PR 10-SEP-1999; 99US-0153406P.  
 PR 15-OCT-1999; 99US-0159783P.  
 XX  
 PA (CONJ-) CONJUCHEM INC.  
 XX  
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 XX  
 DR WPI; 2001-112059/12.  
 XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity.  
 XX  
 PS Disclosure; Page 397; 733pp; English.  
 XX  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide) and maleimide groups) attached to  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 27; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PFGLM 5  
 Db |||||  
 1 PFGLM 5  
 RESULT 16  
 ABB10088  
 ID ABB10088 standard; peptide; 5 AA.  
 XX  
 AC ABB10088;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Substance P analog used in wound healing treatment#11.  
 XX  
 KW Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;  
 KW surgical incision; burn.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200213853-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-JP006933.  
 XX  
 PR 10-AUG-2000; 2000JP-00242489.  
 PR 28-NOV-2000; 2000JP-00361388.

XX (SANT) SANTEN PHARM CO LTD.  
 PA (NISH/) NISHIDA T.  
 XX  
 PI Nishida T, Nakata K, Nakamura M;  
 XX  
 DR WPI; 2002-269153/31.  
 XX  
 PT Skin wound healing promoters or skin epidermal extension promoters  
 PT containing substance P analogs and insulin-like growth factor-I for  
 PT treating wounds like tear, abrasion, surgical incision, skin ulcers or  
 PT burns.  
 XX  
 PS Disclosure; Page 4; 20pp; Japanese.  
 XX  
 CC The invention relates to skin wound healing promoters, containing  
 CC substance P analogs or their pharmaceutically-acceptable salts, and  
 CC insulin-like growth factor-I as the active ingredient. The promoters are  
 CC for treating wounds like tears, abrasions, surgical incisions, or skin  
 CC ulcers and burns. The current sequence represents a substance P analog  
 CC for use in wound healing treatment  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 27; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PFGLM 5  
 Db |||||  
 1 PFGLM 5  
 RESULT 17  
 AAU77845  
 ID AAU77845 standard; peptide; 5 AA.  
 XX  
 AC AAU77845;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Tachykinin N-terminal pentapeptide.  
 XX  
 KW Tachykinin; substance P; hypertension; hypotensive; antidiabetic;  
 KW gynaecological; salt-insensitive hypertension; magnesium binding;  
 KW insulin resistance; type 2 diabetes mellitus; pre-eclampsia; eclampsia.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 5..5  
 FT /note= "C terminal-amide"  
 XX  
 PN WO200211714-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 09-AUG-2001; 2001WO-US024909.  
 XX  
 PR 09-AUG-2000; 2000US-00635266.  
 XX  
 PA (MAGN-) MAGNESIUM DIAGNOSTICS INC.  
 XX  
 PI Wells IC;  
 XX  
 DR WPI; 2002-280663/32.  
 XX  
 PT New monopeptides derived from butadienes, ethylenes and propanes are  
 PT magnesium binding defect antagonists, useful in the treatment of e.g.  
 PT hypertension, insulin resistance of type 2 diabetes mellitus and  
 PT eclampsia.  
 XX  
 PS Disclosure; Page 2; 38pp; English.

XX This invention relates to novel therapeutic compounds and methods used  
 CC for treating mammals with disorders such as salt-insensitive  
 CC hypertension. The mono-peptide compounds of the invention are derived from  
 CC butadienes, ethylenes and propanes. The compounds of the invention are  
 CC used to correct a defect in magnesium binding within the plasma membranes  
 CC of somatic cells which results in a decrease in the intracellular  
 CC concentration of magnesium ions. These compounds may be used in the  
 CC treatment of a mammal affected with magnesium binding defect, salt-  
 CC sensitive (particularly hypertension), insulin resistance of type 2  
 CC diabetes mellitus and pre-eclampsia/eclampsia. The compounds of the  
 CC invention have an advantage over prior art compounds in that these  
 CC compounds are biologically stable. The present sequence represents the a  
 CC pentapeptide from the C-terminal sequence of tachykinin known as  
 CC substance P, this peptide is sufficient to correct the magnesium binding  
 CC defect responsible for causing hypertension  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5  
 |||||  
 Db 1 PFGLM 5

RESULT 18  
 ADE94203  
 ID ADE94203 standard; peptide; 5 AA.

XX ADE94203;

DT 12-FEB-2004 (first entry)

DE High activity minimal IGF-1-derived peptide fragment #15.

KW ophthalmological; dermatological; vulnery; insulin growth factor 1;  
 KW IGF-1; ophthalmology; dermatology; keratic injury; wound healing; skin;  
 KW corneal ulcer; exfoliation of corneal epithelium; keratitis; dry eye;  
 KW scratch; surgical cutting; skin ulcer; burns.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 5 /note= "amidated C-terminus"

PN WO2003048192-A1.

XX 12-JUN-2003.

PF 03-DEC-2002; 2002WO-JP012632.

PR 03-DEC-2001; 2001JP-00368103.

XX (SANT ) SANTEN PHARM CO LTD.

PA (NISH/) NISHIDA T.

PI Nishida T, Inui M, Nakamura M;

XX WPI; 2003-505280/47.

XX Novel peptides based on minimum activity expression units of insulin-like  
 PT growth factor-1, applicable in remedies in ophthalmology and dermatology  
 PT for treating keratic injury and promoting wound healing in skin.

XX Disclosure; Page 7; 25pp; Japanese.

XX The invention relates to the determination of the smallest peptide  
 CC fragment of insulin growth factor 1 (IGF-1) with the highest activity for  
 CC use in ophthalmology and dermatology. The peptides are applicable in

CC remedies in ophthalmology and dermatology for treating keratic injury and  
 CC promoting wound healing in the skin. The keratic injury is particularly  
 CC corneal ulcer, exfoliation of corneal epithelium, keratitis or dry eye.  
 CC The skin wound can be scratches, surgical cutting, skin ulcer, or burns.  
 CC This sequence represents one of the peptides of the invention with IGF-1  
 CC activity.

SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 7; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5  
 |||||  
 Db 1 PFGLM 5

RESULT 19

ADF92530

ID ADF92530 standard; peptide; 5 AA.

XX ADF92530;

DT 26-FEB-2004 (first entry)

DE Substance P receptor agonist #3.

KW analgesic; Mu-opioid receptor agonist; substance P receptor agonist;  
 KW chimeric hybrid; cyclic alkaloid moiety; mu opioid receptor; substance P;  
 KW opioid tolerance; morphine; substance P; SP; neuro-peptide;  
 KW blood-brain barrier; morphine 6-glucuronide; pain; drug abuse; analgesia;  
 KW tolerance development; dependence formation;  
 KW substance P receptor agonist.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 5 /note= "C-terminal amide"

PN US2003202981-A1.

XX 30-OCT-2003.

PF 26-APR-2002; 2002US-00134187.

PR 26-APR-2002; 2002US-00134187.

XX (KREA/) KREAM R M.

XX Kream RM;

XX WPI; 2003-900618/82.

XX Chimeric hybrid molecule useful for treating pain comprising cyclic  
 PT alkaloid moiety which binds as agonist to mammalian mu opioid  
 PT receptor and peptide moiety which binds as agonist to mammalian substance  
 PT P.

XX Claim 7; Page 7; 11pp; English.

XX The invention describes a chimeric hybrid molecule (I) of a cyclic  
 CC alkaloid moiety which binds as an agonist to a mammalian/human mu opioid  
 CC receptor and a peptide moiety which binds as an agonist to a  
 CC mammalian/human substance P. (I) is useful for inhibiting development of  
 CC opioid tolerance by chemically combining a pharmacologically active form  
 CC of substance P with morphine in (I). (I) is useful for transporting an  
 CC active form of SP or neuro-peptide across the blood-brain barrier into the  
 CC central nervous system using the active metabolite of morphine, morphine  
 CC 6-glucuronide, contained in (I). (I) is useful for targeted drug delivery  
 CC of reciprocally regulating analgesic chemicals across the blood-brain  
 CC barrier into the central nervous system using (I). (I) is useful for

CC treating pain in a mammal and for treating drug abuse in a mammal by  
 CC administering (I) in substitution for the drug on which the mammal became  
 CC dependent and/or tolerant and thereafter adjusting the dosage as  
 CC tolerance and/or dependence is modulated. (I) induces analgesia in a  
 CC mammal with tolerance development markedly less than that of morphine.  
 CC (I) efficiently modulates the activation of the MOR and to reduce or  
 CC eliminate tolerance development and dependence formation. This is the  
 CC amino acid sequence of a peptide that functions as a substance P receptor  
 CC agonist.  
 CC  
 XX SQ Sequence 5 AA;  
 CC  
 CC Query Match 100.0%; Score 27; DB 7; Length 5;  
 CC Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 QY 1 FFGLM 5  
 Db |||||  
 1 FFGLM 5  
 CC  
 CC RESULT 20  
 CC ADN95078  
 CC ID ADN95078 standard; peptide; 5 AA.  
 CC  
 CC AC ADN95078;  
 CC  
 CC XX 26-AUG-2004 (first entry)  
 CC DT  
 CC XX Mammalian substance P peptide (amino acids 7-11).  
 CC DE  
 CC XX Opioid tolerance; substance P; morphine; cyclic alkaloid; mammalian;  
 CC KW mu opioid receptor; acute pain; chronic pain; drug abuse;  
 CC KW opioid analgesia; analgesic; antiaddictive.  
 CC XX Mammalia.  
 CC OS  
 CC XX  
 CC PH Key Location/Qualifiers  
 CC FT Modified-site 5 /note= "C-terminal amide"  
 CC FT  
 CC PN US2004106636-A1.  
 CC XX  
 CC PD 03-JUN-2004.  
 CC XX  
 CC PF 17-OCT-2003; 2003US-00688741.  
 CC XX  
 CC PR 26-APR-2002; 2002US-00134187.  
 CC XX  
 CC PA (KREA/) KREAM R M.  
 CC XX  
 CC PI Kream RM;  
 CC XX  
 CC DR WPI; 2004-419489/39.  
 CC XX  
 CC PT Inhibiting development of opioids tolerance involves use of chimeric  
 CC PT hybrid molecules containing an opioid moiety of chemically modified  
 CC PT morphine.  
 CC  
 CC XX Disclosure; SEQ ID NO 3; 10pp; English.  
 CC  
 CC The present invention relates to a method of inhibiting the development  
 CC of opioid tolerance. The method involves administering a chemical  
 CC combination of an active form of substance P with morphine in a new  
 CC chimeric hybrid molecule. The morphine is chemically modified and  
 CC covalently linked through its 6'OH group, and comprises a cyclic alkaloid  
 CC moiety which binds as an agonist to a mammalian or human mu opioid  
 CC receptor. An active C-mu terminal substance P fragment, chemically  
 CC modified and covalently linked through its free NH2 group, comprises a  
 CC peptide moiety, which binds moiety which binds as an agonist to a  
 CC mammalian/human substance P receptor. A compact, but flexible, molecular  
 CC hinge covalently cross links morphine through its 6'OH group to the free  
 CC NH2 group of the substance P receptor agonist moiety, so as to allow both

CC the mu opioid receptor and the substance P receptor agonist moieties to  
 CC activate their respective receptors simultaneously and independently. The  
 CC chimeric hybrid molecules are administered intrathecally, systemically,  
 CC orally, intradermally, parenterally (e.g. subcutaneously, intravenously),  
 CC through injection, transdermally, (e.g. topically), transmucosally or  
 CC rectally. The method is useful for the treatment of acute and chronic  
 CC pain, and drug abuse. The molecules show reduced side effects. The  
 CC molecules provide opioid analgesia in living subjects while inhibiting  
 CC tolerance development and dependence formation. The present sequence  
 CC representing a peptide from mammalian substance P is used in the method  
 CC of the invention.  
 CC  
 XX SQ Sequence 5 AA;  
 CC  
 CC Query Match 100.0%; Score 27; DB 8; Length 5;  
 CC Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 QY 1 FFGLM 5  
 Db |||||  
 1 FFGLM 5  
 CC  
 CC RESULT 21  
 CC ADR43771  
 CC ID ADR43771 standard; peptide; 5 AA.  
 CC  
 CC AC ADR43771;  
 CC  
 CC XX 19-NOV-2004 (first entry)  
 CC DT  
 CC XX Human magnesium binding defect (MgBD) peptide mimetic #1.  
 CC DE  
 CC XX Magnesium binding defect; MgBD; MgBD binding defect peptide mimetic;  
 CC KW physiological disorder; preclampsia; pregnancy;  
 CC KW salt-sensitive essential hypertension; type 2 diabetes mellitus; human.  
 CC XX  
 CC OS Homo sapiens.  
 CC XX  
 CC PH Key Location/Qualifiers  
 CC FT Modified-site 5 /label= OTHER  
 CC FT /note= "OTHER= C-terminal amide"  
 CC FT  
 CC PN US2004171093-A1.  
 CC XX  
 CC PD 02-SEP-2004.  
 CC XX  
 CC PF 22-MAR-2004; 2004US-00805881.  
 CC XX  
 CC PR 10-MAR-1999; 99US-00265690.  
 CC PR 09-AUG-2000; 2000US-00635266.  
 CC PR 24-JAN-2002; 2002US-00053669.  
 CC PR 29-AUG-2002; 2002US-00230133.  
 CC PR 28-OCT-2003; 2003US-00695536.  
 CC XX  
 CC PA (WELL/) WELLS I C.  
 CC XX  
 CC PI Wells IC;  
 CC XX  
 CC DR WPI; 2004-625105/60.  
 CC  
 CC PT Assessing predisposition to physiological disorder associated with  
 CC PT magnesium binding defect in individual, by measuring level of amidated  
 CC PT peptides associated with magnesium binding defect in sample and comparing  
 CC PT peptide level to standard.  
 CC XX  
 CC PS Claim 1; SEQ ID NO 1; 21pp; English.  
 CC  
 CC The invention relates to a method of assessing a predisposition to a  
 CC physiological disorder associated with a magnesium binding defect in an  
 CC individual, involving measuring the level of amidated peptides associated  
 CC with the magnesium binding defect in a sample of body fluid of the



CC individual and comparing the level of peptide to a standard, where a  
 CC significantly lower level of the peptide is indicative of a  
 CC predisposition of the individual to the physiological disorder. The  
 CC invention also relates to a method of monitoring progress in treatment of  
 CC a physiological disorder associated with a magnesium binding defect in an  
 CC individual, involving comparing the level of peptide to the level of  
 CC peptide after treatment, where a significant increase in the level of the  
 CC peptide is indicative of the progress of treatment of the individual, a  
 CC monoclonal antibody that specifically binds to a peptide or its peptide  
 CC mimetic, a prognosis reagent for determining the presence of a magnesium  
 CC binding defect, generating a deficit of plasma membrane tightly bound  
 CC magnesium ion in mammalian somatic cells involving obtaining a sample of  
 CC body fluid comprising somatic cells, collecting the somatic cells from  
 CC the body fluid by centrifugation, resuspending the somatic cells in a  
 CC cell stabilising buffer, removing a sample of the suspended somatic  
 CC cells, measuring the level of tightly bound magnesium ion in the sample  
 CC of the somatic cells and repeating the removing and measuring steps at  
 CC subsequent times until the level of tightly bound magnesium is  
 CC significantly reduced and the somatic cells remain intact, a method of  
 CC identifying substances which promote binding of tightly bound magnesium  
 CC ion to a plasma membrane of mammalian somatic cells involving suspending  
 CC mammalian somatic cells having a deficit of plasma membrane tightly bound  
 CC magnesium in a physiological medium including magnesium ion, adding a  
 CC substance to be tested to the suspension and measuring the level of  
 CC tightly bound magnesium ion in the plasma membrane of the somatic cells  
 CC where a significant increase in the level of plasma membrane tightly  
 CC bound magnesium after addition of the substance to be tested is  
 CC indicative of promotion of binding by the substance, and a method for  
 CC ameliorating or correcting a magnesium binding defect in an individual  
 CC involving administering to the individual a substance which promotes  
 CC binding of tightly bound magnesium ion to the plasma membrane of  
 CC mammalian somatic cells. The methods are useful for assessing a  
 CC predisposition to a physiological disorder associated with a magnesium  
 CC binding defect in an individual, where the disorder is a predisposition  
 CC to preeclampsia during pregnancy, salt-sensitive essential hypertension  
 CC or type 2 diabetes mellitus associated with the magnesium binding defect.  
 CC The method is also useful for ameliorating or correcting a magnesium  
 CC binding defect (MgBD) in an individual. This sequence represents a human  
 CC MgBD mimetic peptide of the invention.

XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FFGLM 5  
 |||||  
 Db 1 FFGLM 5

Search completed: March 23, 2005, 15:32:58  
 Job time : 73 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:50:07 ; Search time 92 Seconds  
(without alignments)  
17.995 Million cell updates/sec

Title: SEQ1

Perfect score: 27

Sequence: 1 ffglm 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 21937

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pap.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pap.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pap.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	27	100.0	5	9	US-09-265-690C-1
2	27	100.0	5	14	US-10-053-669-1
3	27	100.0	5	15	US-10-134-187-3
4	27	100.0	5	16	US-10-688-741-3
5	27	100.0	5	16	US-10-805-881-1
6	27	100.0	5	17	US-10-497-628-15
7	24	88.9	5	17	US-10-497-628-16
8	22	81.5	4	17	US-10-821-240A-270
9	21	77.8	4	9	US-09-265-690C-2
10	21	77.8	4	14	US-10-230-133-3
11	21	77.8	4	14	US-10-053-669-2
12	21	77.8	4	16	US-10-695-536-3
13	21	77.8	4	16	US-10-805-881-2

14	21	77.8	4	17	US-10-497-628-2	Sequence 2, Appli
15	21	77.8	5	16	US-10-346-737A-30	Sequence 30, Appli
16	21	77.8	5	17	US-10-497-628-17	Sequence 17, Appli
17	20	74.1	5	9	US-09-265-690C-4	Sequence 4, Appli
18	20	74.1	5	14	US-10-230-133-4	Sequence 4, Appli
19	20	74.1	5	14	US-10-053-669-4	Sequence 4, Appli
20	20	74.1	5	16	US-10-695-536-4	Sequence 4, Appli
21	20	74.1	5	16	US-10-805-881-4	Sequence 4, Appli
22	19	70.4	5	16	US-10-346-737A-22	Sequence 22, Appli
23	18	66.7	4	8	US-08-484-409-14	Sequence 14, Appli
24	18	66.7	4	14	US-10-155-170-4	Sequence 4, Appli
25	18	66.7	4	14	US-10-351-641-826	Sequence 826, App
26	18	66.7	4	16	US-10-822-661-4	Sequence 4, Appli
27	18	66.7	4	17	US-10-821-240A-298	Sequence 298, App
28	18	66.7	5	11	US-09-920-306-38	Sequence 38, Appli
29	17	63.0	5	14	US-10-168-789A-32	Sequence 32, Appli
30	17	63.0	5	17	US-10-783-311-299	Sequence 299, App
31	16	59.3	4	9	US-09-879-442A-9	Sequence 9, Appli
32	16	59.3	5	10	US-09-886-135-2	Sequence 2, Appli
33	16	59.3	5	16	US-10-820-052A-45	Sequence 45, Appli
34	16	59.3	5	16	US-10-337-105-3	Sequence 3, Appli
35	16	59.3	5	16	US-10-337-105-4	Sequence 4, Appli
36	16	59.3	5	17	US-10-891-122-2	Sequence 2, Appli
37	15	55.6	3	14	US-10-230-133-2	Sequence 2, Appli
38	15	55.6	3	16	US-10-695-536-2	Sequence 2, Appli
39	15	55.6	4	17	US-10-823-964A-11	Sequence 11, Appli
40	15	55.6	5	11	US-09-920-306-40	Sequence 40, Appli
41	15	55.6	5	14	US-10-301-499A-25	Sequence 25, Appli
42	15	55.6	5	14	US-10-168-789A-39	Sequence 39, Appli
43	15	55.6	5	14	US-10-194-441A-85	Sequence 85, Appli
44	15	55.6	5	15	US-10-311-366-9	Sequence 9, Appli
45	15	55.6	5	16	US-10-128-520-360	Sequence 360, App

#### ALIGNMENTS

RESULT 1  
US-09-265-690C-1  
; Sequence 1, Application US/09265690C  
; Publication No. US20010051345A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound M  
; FILE REFERENCE: 1427001  
; CURRENT APPLICATION NUMBER: US/09/265,690C  
; CURRENT FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: AMIDATION  
US-09-265-690C-1

Query Match 100.0%; Score 27; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFGLM 5

Db 1 FFGLM 5

RESULT 2

US-10-053-669-1

; Sequence 1, Application US/10053669

; Publication No. US20030077659A1

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; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-10-053-669-1

Query Match
Best Local Similarity 100.0%; Score 27; DB 14; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
DB 1 FFGLM 5

RESULT 3
US-10-134-187-3
; Sequence 3, Application US/10134187
; Publication NO. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Chimeric Hybrid Analgesics
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/134,187
; CURRENT FILING DATE: 2002-04-26
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-10-134-187-3

Query Match
Best Local Similarity 100.0%; Score 27; DB 15; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
DB 1 FFGLM 5

RESULT 4
US-10-688-741-3
; Sequence 3, Application US/10688741
; Publication NO. US20040106636A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric H
; FILE REFERENCE: Kream
; CURRENT APPLICATION NUMBER: US/10/688,741
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 3
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mammalian
US-10-688-741-3

Query Match
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
DB 1 FFGLM 5

RESULT 5
US-10-805-881-1
; Sequence 1, Application US/10805881
; Publication NO. US20040171093A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert C.
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
; FILE REFERENCE: 800812-0005
; CURRENT APPLICATION NUMBER: US/10/805,881
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 10/053,669
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 10/695,536
; PRIOR FILING DATE: 2003-10-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-10-805-881-1

Query Match
Best Local Similarity 100.0%; Score 27; DB 16; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFGLM 5
DB 1 FFGLM 5

RESULT 6
US-10-497-628-15
; Sequence 15, Application US/10497628
; Publication NO. US20050009752A1
; GENERAL INFORMATION:
; APPLICANT: Teruo Nishida
; APPLICANT: Makoto Inui
; APPLICANT: Masatsugu Nakamura
; TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
; FILE REFERENCE: 04355/HG
; CURRENT APPLICATION NUMBER: US/10/497,628
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: JP 2001-368103
; PRIOR FILING DATE: 2001-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-10-497-628-15
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5  
Db 1 PFGLM 5

## RESULT 7

US-10-497-628-16  
; Sequence 16, Application US/10497628  
; Publication No. US20050009752A1  
; GENERAL INFORMATION:  
; APPLICANT: Teruo Nishida  
; APPLICANT: Makoto Inui  
; APPLICANT: Masatugu Nakamura  
; TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME  
; FILE REFERENCE: 04355/HG  
; CURRENT APPLICATION NUMBER: US/10/497,628  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: JP 2001-368103  
; PRIOR FILING DATE: 2001-12-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-497-628-16

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Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5  
Db 1 YFGLM 5

## RESULT 8

US-10-821-240A-270  
; Sequence 270, Application US/10821240A  
; Publication No. US20050037430A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Bennex, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/821,240A  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: 10/028,075  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 312  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 270  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: derivative peptide based on m  
; OTHER INFORMATION: metalloproteinase-2  
US-10-821-240A-270

Query Match 81.5%; Score 22; DB 17; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGL 4  
||||

Db 1 PFGL 4

## RESULT 9

US-09-265-690C-2  
; Sequence 2, Application US/09265690C  
; Publication No. US20010051345A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound M  
; FILE REFERENCE: 1427001  
; CURRENT APPLICATION NUMBER: US/09/265,690C  
; CURRENT FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: AMIDATION  
US-09-265-690C-2

Query Match 77.8%; Score 21; DB 9; Length 4;  
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Qy 2 FGLM 5  
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Db 1 FGLM 4

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US-10-230-133-3  
; Sequence 3, Application US/10230133  
; Publication No. US20030040625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents an  
; FILE REFERENCE: 2892-106  
; CURRENT APPLICATION NUMBER: US/10/230,133  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 09/635,266  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: AMIDATION  
US-10-230-133-3

Query Match 77.8%; Score 21; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
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Qy 2 FGLM 5  
||||  
Db 1 FGLM 4

## RESULT 11

US-10-053-669-2  
; Sequence 2, Application US/10053669  
; Publication No. US20030077658A1

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/ GENERAL INFORMATION:
/ APPLICANT: Wells, Ibert
/ TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
/ TITLE OF INVENTION: for Disease Diagnosis
/ FILE REFERENCE: N1427-005
/ CURRENT APPLICATION NUMBER: US/10/053,669
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: 09/265,690
/ PRIOR FILING DATE: 1999-03-10
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: AMIDATION
/ US-10-053-669-2

Query Match          77.8%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FGLM 5
Db      1 FGLM 4

RESULT 12
US-10-695-536-3
/ Sequence 3, Application US/10695536
/ Publication No. US20040110692A1
/ GENERAL INFORMATION:
/ APPLICANT: Wells, Ibert Clifton
/ TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
/ TITLE OF INVENTION: and Methods for Treatment of Abnormal Physiological States
/ FILE REFERENCE: 800812-0008
/ CURRENT APPLICATION NUMBER: US/10/695,536
/ CURRENT FILING DATE: 2003-10-28
/ PRIOR APPLICATION NUMBER: US 10/230,133
/ PRIOR FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: US 09/635,266
/ PRIOR FILING DATE: 2000-08-09
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: AMIDATION
/ US-10-695-536-3

Query Match          77.8%; Score 21; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FGLM 5
Db      1 FGLM 4

RESULT 13
US-10-805-881-2
/ Sequence 2, Application US/10805881
/ Publication No. US2004011093A1
/ GENERAL INFORMATION:
/ APPLICANT: Wells, Ibert C.
/ TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
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/ TITLE OF INVENTION: Magnesium for Disease Diagnosis
/ FILE REFERENCE: 800812-0005
/ CURRENT APPLICATION NUMBER: US/10/805,881
/ CURRENT FILING DATE: 2004-03-22
/ PRIOR APPLICATION NUMBER: US 10/053,669
/ PRIOR FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: US 10/695,536
/ PRIOR FILING DATE: 2003-10-28
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: AMIDATION
/ US-10-805-881-2

Query Match          77.8%; Score 21; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FGLM 5
Db      1 FGLM 4

RESULT 14
US-10-497-628-2
/ Sequence 2, Application US/10497628
/ Publication No. US20050009752A1
/ GENERAL INFORMATION:
/ APPLICANT: Teruo Nishida
/ APPLICANT: Makoto Inui
/ APPLICANT: Masatsugu Nakamura
/ TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
/ FILE REFERENCE: 04355/HG
/ CURRENT APPLICATION NUMBER: US/10/497,628
/ CURRENT FILING DATE: 2004-06-03
/ PRIOR APPLICATION NUMBER: JP 2001-368103
/ PRIOR FILING DATE: 2001-12-01
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Human
/ US-10-497-628-2

Query Match          77.8%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FGLM 5
Db      1 FGLM 4

RESULT 15
US-10-346-737A-30
/ Sequence 30, Application US/10346737A
/ Publication No. US20040142379A1
/ GENERAL INFORMATION:
/ APPLICANT: St. Hilaire, Phaedria
/ TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS
/ FILE REFERENCE: 11225.16US01
/ CURRENT APPLICATION NUMBER: US/10/346,737A
/ CURRENT FILING DATE: 2003-01-16
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30
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; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: Xaa is T(Sa)  
US-10-346-737A-30

Query Match 77.8%; Score 21; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FGLM 5  
|  
|  
|  
|  
Db 2 FGLM 5

Search completed: March 23, 2005, 15:07:05  
Job time : 92 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:37:21 ; Search time 30 Seconds  
(without alignments)  
12.442 Million cell updates/sec

Title: SEQ1  
Perfect score: 27  
Sequence: 1 ffglm 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 27945

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgm2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgm2\_6/ptodata/1/iaa/PCUS\_COMB.pep:\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	5	1 US-07-934-553-2	Sequence 2, Appli
2	27	100.0	5	1 US-08-225-474-2	Sequence 2, Appli
3	27	100.0	5	2 US-07-737-371E-6	Sequence 6, Appli
4	27	100.0	5	3 US-09-265-690C-1	Sequence 1, Appli
5	24	88.9	5	2 US-07-737-371E-48	Sequence 48, Appli
6	22	81.5	5	2 US-07-737-371E-47	Sequence 47, Appli
7	22	81.5	5	2 US-07-737-371E-49	Sequence 49, Appli
8	21	77.8	4	1 US-08-441-591-63	Sequence 63, Appli
9	21	77.8	4	1 US-08-303-362A-63	Sequence 63, Appli
10	21	77.8	4	3 US-09-265-690C-2	Sequence 2, Appli
11	21	77.8	4	4 US-09-635-266-3	Sequence 3, Appli
12	21	77.8	4	4 US-10-230-133-3	Sequence 3, Appli
13	21	77.8	4	5 PCT-US95-05600-80	Sequence 80, Appli
14	21	77.8	5	2 US-08-070-301-6	Sequence 6, Appli
15	20	74.1	5	1 US-07-753-909B-3	Sequence 3, Appli
16	20	74.1	5	1 US-08-269-288-1	Sequence 1, Appli
17	20	74.1	5	1 US-08-391-910-1	Sequence 1, Appli
18	20	74.1	5	1 US-08-418-994-1	Sequence 1, Appli
19	20	74.1	5	1 US-08-391-814-1	Sequence 1, Appli
20	20	74.1	5	1 US-08-441-591-61	Sequence 61, Appli
21	20	74.1	5	1 US-08-303-362A-61	Sequence 61, Appli
22	20	74.1	5	1 US-08-462-415-1	Sequence 1, Appli
23	20	74.1	5	1 US-08-463-874-1	Sequence 1, Appli
24	20	74.1	5	1 US-08-444-135-1	Sequence 1, Appli
25	20	74.1	5	1 US-08-318-391-1	Sequence 1, Appli
26	20	74.1	5	3 US-08-257-966-1	Sequence 1, Appli
27	20	74.1	5	3 US-09-265-690C-4	Sequence 4, Appli

28	20	74.1	5	4 US-08-153-847-1	Sequence 1, Appli
29	20	74.1	5	4 US-09-635-266-4	Sequence 4, Appli
30	20	74.1	5	4 US-10-230-133-4	Sequence 4, Appli
31	20	74.1	5	5 PCT-US95-05600-78	Sequence 78, Appli
32	19	70.4	4	3 US-08-722-126A-20	Sequence 20, Appli
33	19	70.4	5	2 US-08-765-061-5	Sequence 5, Appli
34	18	66.7	4	1 US-07-822-924-7	Sequence 7, Appli
35	18	66.7	4	1 US-08-285-777-1	Sequence 1, Appli
36	18	66.7	4	1 US-08-127-904-11	Sequence 11, Appli
37	18	66.7	4	1 US-08-431-539-4	Sequence 4, Appli
38	18	66.7	4	2 US-09-060-455-16	Sequence 16, Appli
39	18	66.7	4	3 US-09-082-279B-826	Sequence 826, Appli
40	18	66.7	4	3 US-09-264-709A-12	Sequence 12, Appli
41	18	66.7	4	3 US-09-264-709A-18	Sequence 18, Appli
42	18	66.7	4	3 US-09-264-709A-19	Sequence 19, Appli
43	18	66.7	4	3 US-09-264-709A-23	Sequence 23, Appli
44	18	66.7	4	3 US-09-264-709A-24	Sequence 24, Appli
45	18	66.7	4	3 US-09-264-709A-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1  
US-07-934-553-2  
; Sequence 2, Application US/07934553  
; Patent No. 5314690  
; GENERAL INFORMATION:  
; APPLICANT: PATTERSON, ROY  
; APPLICANT: HARRIS, KATHLEEN E  
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: TILTON, FALLON, LUNGUMUS & CHESTNUT  
; STREET: 100 SOUTH WACKER DRIVE  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60606-4002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934.553  
; FILING DATE: 19920821  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/705.071  
; FILING DATE: 24-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PENTRESS, SUSAN B  
; REGISTRATION NUMBER: 31,327  
; REFERENCE/DOCKET NUMBER: NU-9033CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/456-8000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-07-934-553-2

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PFGLM 5  
|||||

Db 1 FFGLM 5

## RESULT 2

US-08-225-474-2  
; Sequence 2, Application US/08225474  
; Patent No. 5560915  
; GENERAL INFORMATION:  
; APPLICANT: Patterson, Roy  
; APPLICANT: Harris, Kathleen E.  
; TITLE OF INVENTION: Method and Composition for Treating  
; TITLE OF INVENTION: Ige Mediated Allergies  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut  
; STREET: 100 S. Wacker Drive, Suite 960  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-4002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,474  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,553  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/705,071  
; FILING DATE: 24-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tilton, Timothy L.  
; REGISTRATION NUMBER: 16,926  
; REFERENCE/DOCKET NUMBER: NU 9033-CIP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)-456-8000  
; TELEFAX: (312)-456-7776  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-225-474-2

Query Match 100.0%; Score 27; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFGLM 5

Db 1 FFGLM 5

## RESULT 3

US-07-737-371E-6  
; Sequence 6, Application US/07737371E  
; Patent No. 5876948  
; GENERAL INFORMATION:  
; APPLICANT: Yankner, Bruce A.  
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY  
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston

STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/737,371E  
FILING DATE: 29-JUL-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/559,172  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00108/028002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-737-371E-6

Query Match 100.0%; Score 27; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFGLM 5

Db 1 FFGLM 5

## RESULT 4

US-09-265-690C-1  
; Sequence 1, Application US/09265690C  
; Patent No. 6372440  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound M  
; TITLE OF INVENTION: for Disease Diagnosis  
; FILE REFERENCE: 1427001  
; CURRENT APPLICATION NUMBER: US/09/265,690C  
; CURRENT FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (5)-(5)  
; OTHER INFORMATION: AMIDATION  
US-09-265-690C-1

Query Match 100.0%; Score 27; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFGLM 5

Db 1 FFGLM 5

## RESULT 5

```

US-07-737-371E-48
; Sequence 48, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-8906
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 5...5
; OTHER INFORMATION: where Xaa at position 5 is Nle
US-07-737-371E-48

```

```

Query Match      88.9%; Score 24; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 PFGLM 5
        :|||
Db      1 YFGLM 5

```

```

RESULT 6
US-07-737-371E-47
; Sequence 47, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-8906
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 5...5
; OTHER INFORMATION: where Xaa at position 5 is Nle
US-07-737-371E-47

```

```

Query Match      81.5%; Score 22; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 PFGL 4
        :|||
Db      1 PFGL 4

```

```

RESULT 7
US-07-737-371E-49
; Sequence 49, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-8906
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
LOCATION: 5...5

OTHER INFORMATION: where Xaa at position 5 is ethionine  
US-07-737-371E-49

Query Match 81.5%; Score 22; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PFGL 4  
DB 1 PFGL 4

## RESULT 8

US-08-441-591-63  
Sequence 63, Application US/08441591  
Patent No. 5637682  
GENERAL INFORMATION:  
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
TITLE OF INVENTION: HIGH-AFFINITY  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
TITLE OF INVENTION: TO THE TACHYKININ  
TITLE OF INVENTION: SUBSTANCE P  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION NUMBER: US/08/441,591  
FILING DATE: 9-SEPTEMBER-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/303,362  
FILING DATE: 9-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 8-SEPTEMBER 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX21/C  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4

Query Match 77.8%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-441-591-63

Query Match 77.8%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGLM 5  
DB 1 FGLM 4

## RESULT 9

US-08-303-362A-63  
Sequence 63, Application US/08303362A  
Patent No. 5648214  
GENERAL INFORMATION:  
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
TITLE OF INVENTION: HIGH-AFFINITY  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
TITLE OF INVENTION: TO THE TACHYKININ  
TITLE OF INVENTION: SUBSTANCE P  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION NUMBER: US/08/303,362A  
FILING DATE: 9-SEPTEMBER-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 8-SEPTEMBER 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX21  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-303-362A-63

Query Match 77.8%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGLM 5  
Db 1 FGLM 4

## RESULT 10

US-09-265-690C-2

; Sequence 3, Application US/09265690C

; Patent No. 6372440

; GENERAL INFORMATION:

; APPLICANT: Wells, Ibert

; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma

; FILE REFERENCE: 1427001

; CURRENT APPLICATION NUMBER: US/09/265,690C

; CURRENT FILING DATE: 1999-03-10

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD\_RES

; LOCATION: (4)..(4)

; OTHER INFORMATION: AMIDATION

US-09-265-690C-2

## Query Match

Best Local Similarity 77.8%; Score 21; DB 3; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGLM 5  
Db 1 FGLM 4

## RESULT 11

US-09-635-266-3

; Sequence 3, Application US/09635266

; Patent No. 6455734

; GENERAL INFORMATION:

; APPLICANT: Wells, Ibert

; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and

; FILE REFERENCE: N1427-002

; CURRENT APPLICATION NUMBER: US/09/635,266

; CURRENT FILING DATE: 2000-08-09

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD\_RES

; LOCATION: (4)..(4)

; OTHER INFORMATION: AMIDATION

US-09-635-266-3

## Query Match

Best Local Similarity 77.8%; Score 21; DB 4; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGLM 5  
Db 1 FGLM 4

## RESULT 12

US-10-230-133-3

; Sequence 3, Application US/10230133

; Patent No. 6664420

; GENERAL INFORMATION:

; APPLICANT: Wells, Ibert

; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents an

; FILE REFERENCE: 2892-106

; CURRENT APPLICATION NUMBER: US/10/230,133

; CURRENT FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: 09/635,266

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD\_RES

; LOCATION: (4)..(4)

; OTHER INFORMATION: AMIDATION

US-10-230-133-3

## Query Match

Best Local Similarity 77.8%; Score 21; DB 4; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGLM 5  
Db 1 FGLM 4

## RESULT 13

PCT-US95-05600-80

; Sequence 80, Application PC/TUS9505600

; GENERAL INFORMATION:

; APPLICANT: GOLD, LARRY

; APPLICANT: NIEUMLANDT, DAN

; APPLICANT: WECKER, MATTHEW

; APPLICANT: SCHNEIDER, DANIEL J.

; APPLICANT: FEIGON, JULI

; APPLICANT: ALLEN, PATRICK

; APPLICANT: SULLENGER, BRUCE A.

; APPLICANT: DODNA, JENNIFER, A.

; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF

; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE

; NUMBER OF SEQUENCES: 239

; CORRESPONDENCE ADDRESS: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE

; ADDRESS: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG

; MEDIUM TYPE: storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05600

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION NUMBER: 08/238,863

; FILING DATE: 06-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/248,632

; FILING DATE: 24-MAY-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/303,362
; FILING DATE: 09-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 08-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX17/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-05600-80

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Query Match 77.8%; Score 21; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 FGLM 5
   ||||
Db 1 FGLM 4

```

```

RESULT 14
US-08-070-301-6
; Sequence 6, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Ohji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-106412
; FILING DATE: 24-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-205475
; FILING DATE: 02-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-22830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-040
; TELEFAX: (202) 835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-070-301-6

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```

Query Match 77.8%; Score 21; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 FGLM 5
   ||||
Db 1 FGLM 4

```

```

RESULT 15
US-07-753-909B-3
; Sequence 3, Application US/07753909B
; Patent No. 5304632
; GENERAL INFORMATION:
; APPLICANT: Vaudry, Hubert
; APPLICANT: Conlon, Michael J.
; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zarley, McKee, Thomte, Voorhees, and Sease
; STREET: 801 Grand, Suite 3200
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/753,909B
; FILING DATE: 19910903
; CLASSIFICATION: 530

```

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: FR 9106759  
;; FILING DATE: 04-JUN-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sease, Edmund J.  
;; REGISTRATION NUMBER: 24,741  
;; TELEPHONE: (515)-288-3667  
;; TELEFAX: (515)-288-1338  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 5 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: C-terminal  
;; ORIGINAL SOURCE:  
;; ORGANISM: Rana ridibunda  
;; DEVELOPMENTAL STAGE: adult  
;; TISSUE TYPE: brain  
US-07-753-909B-3

Query Match 74.1%; Score 20; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.le+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 PFGLM 5  
| | | | |  
Db 1 FXGLM 5

Search completed: March 23, 2005, 14:50:58  
Job time : 31 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 14:38:05 ; Search time 23.5 Seconds  
(without alignments)  
20.472 Million cell updates/sec

Title: SEQ2

Perfect score: 25

Sequence: 1 fvglm 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:\*\*

2: Pirl:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	56.0	5	2 G44817	27.5 kda structural p
2	14	56.0	5	2 I44817	27.5K structural p
3	14	56.0	5	2 E44817	27.5K structural p
4	14	56.0	5	2 C44817	28.5K structural p
5	14	56.0	5	2 A44817	28K structural pro
6	11	44.0	4	2 PT0240	Ig heavy chain CRD
7	11	44.0	5	2 A61445	Met-enkephalin - b
8	11	44.0	5	2 PT0278	Ig heavy chain CRD
9	10	40.0	4	2 A53284	T-cell receptor be
10	10	40.0	5	2 B61168	cocoonase (EC 3.4.
11	10	40.0	5	2 A44592	fulicin - giant Af
12	9	36.0	5	2 A32516	cholecystokinin-5
13	9	36.0	5	4 A58728	serrawettin W2 - S
14	8	32.0	4	2 PT0633	T-cell receptor be
15	8	32.0	5	2 A44955	alkanal monooxygen
16	8	32.0	5	2 B61445	Leu-enkephalin - b
17	8	32.0	5	2 PT0572	T-cell receptor be
18	7	28.0	3	3 B23751	spinal cord peptid
19	7	28.0	4	2 T30569	hypothetical prote
20	7	28.0	4	2 I38888	COI intron 16 prot
21	7	28.0	4	2 E44823	synaptosomal-assoc
22	7	28.0	4	2 PL0140	carbon-monoxide de
23	7	28.0	4	2 A35779	neuropeptide Antho
24	7	28.0	4	2 A60418	FMRFamide - polych
25	7	28.0	4	2 PT0721	T-cell receptor be
26	7	28.0	4	2 A32039	tyrosine-melanocyt
27	7	28.0	4	2 ECNK	cardioexcitatory n
28	7	28.0	5	2 T10954	hypothetical prote
29	7	28.0	5	2 B45525	actin I - malaria

30 7 28.0 5 2 D44823 synaptosomal-assoc  
31 7 28.0 5 2 PT0713 T-cell receptor be  
32 7 28.0 5 2 S69237 surface protein te  
33 6 24.0 3 3 PT0636 T-cell receptor be  
34 6 24.0 3 3 PT0571 T-cell receptor be  
35 6 24.0 3 3 S68328 blood cell protein  
36 6 24.0 3 3 GKHU growth-modulating  
37 6 24.0 3 3 A60898 bursin - chicken  
38 6 24.0 3 3 A23751 spinal cord peptid  
39 6 24.0 4 1 BCXAA anho-RFamide neur  
40 6 24.0 4 2 D41654 hypothetical prote  
41 6 24.0 4 2 S53508 starvation-induced  
42 6 24.0 4 2 A25844 auto-RF amide neu  
43 6 24.0 4 2 A34626 RPCH-related neuro  
44 6 24.0 4 2 S39390 myosin-light-chain  
45 6 24.0 4 2 S43959 Ig mu chain V regi

#### ALIGNMENTS

##### RESULT 1

G44817

27.5 kda structural protein - Leuconostoc oenos phase P32 (fragment)

C;Species: Leuconostoc oenos phase P32

C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998

C;Accession: G44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: G44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 56.0%; Score 14; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGL 4

Db 3 VGL 5

##### RESULT 2

I44817

27.5K structural protein - Leuconostoc oenos phase P37 (fragment)

C;Species: Leuconostoc oenos phase P37

C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998

C;Accession: I44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: I44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 56.0%; Score 14; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGL 4

Db 3 VGL 5

##### RESULT 3

E44817

27.5K structural protein - Leuconostoc oenos phase P54 (fragment)

C;Species: Leuconostoc oenos phase P54

C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: E44817  
 R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A;Title: Lysogeny in Leuconostoc oenos.  
 A;Reference number: A44817; PMID:92085033; PMID:1748868  
 A;Accession: E44817  
 A;Molecule type: protein  
 A;Residues: 1-5 <ARE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 56.0%; Score 14; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. NO. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGL 4  
 :|||  
 Db 3 VGL 5

RESULT 4  
 C44817  
 28-K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)  
 C;Species: Leuconostoc oenos phase PAT5-12  
 C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: C44817  
 R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A;Title: Lysogeny in Leuconostoc oenos.  
 A;Reference number: A44817; PMID:92085033; PMID:1748868  
 A;Accession: C44817  
 A;Molecule type: protein  
 A;Residues: 1-5 <ARE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 56.0%; Score 14; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. NO. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGL 4  
 :|||  
 Db 3 VGL 5

RESULT 5  
 A44817  
 28K structural protein - Leuconostoc oenos phase PZt11-15 (fragment)  
 C;Species: Leuconostoc oenos phase PZt11-15  
 C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: A44817  
 R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A;Title: Lysogeny in Leuconostoc oenos.  
 A;Reference number: A44817; PMID:92085033; PMID:1748868  
 A;Accession: A44817  
 A;Molecule type: protein  
 A;Residues: 1-5 <ARE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 56.0%; Score 14; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. NO. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGL 4  
 :|||  
 Db 3 VGL 5

RESULT 6  
 PT0240  
 Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0240  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J.  
 A;Reference number: PT0222; PMID:91108337; PMID:1899102  
 A;Accession: PT0240  
 A;Molecule type: DNA  
 A;Residues: 1-4 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 44.0%; Score 11; DB 2; Length 4;  
 Best Local Similarity 50.0%; Pred. NO. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGL 4  
 :|||  
 Db 1 YFGL 4

RESULT 7  
 A61445  
 Met-enkephalin - blue mussel  
 C;Species: Mytilus edulis (blue mussel)  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C;Accession: A61445  
 R;Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A;Reference number: A61445; PMID:84144823; PMID:6583690  
 A;Accession: A61445  
 A;Molecule type: protein  
 A;Residues: 1-5 <LEU>  
 A;Experimental source: pedal ganglia  
 C;Keywords: neuropeptide; opioid peptide

Query Match 44.0%; Score 11; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. NO. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GLM 5  
 :|||  
 Db 3 GFM 5

RESULT 8  
 PT0278  
 Ig heavy chain CRD3 region (clone 4-88) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0278  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J.  
 A;Reference number: PT0222; PMID:91108337; PMID:1899102  
 A;Accession: PT0278  
 A;Molecule type: DNA  
 A;Residues: 1-5 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 44.0%; Score 11; DB 2; Length 5;  
 Best Local Similarity 20.0%; Pred. NO. 2.8e+05;  
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 :|||  
 Db 1 YFGLV 5

RESULT 9  
 A53284  
 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C;Accession: A53284  
 R;Harindranath, N.; Alexander, C.B.; Mage, R.G.  
 Mol. Immunol. 28, 881-888, 1991  
 A;Title: Evolutionarily conserved organization and sequences of germline diversity and  
 A;Reference number: A53284; MUID:91342695; PMID:1678859  
 A;Accession: A53284  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-4 <HAR>  
 A;Cross-references: GB:S60737; NID:G233917; PID:G233917  
 A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)  
 C;Keywords: T-cell receptor

Query Match 40.0%; Score 10; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GL 4  
 ||  
 1 GL 2

RESULT 10  
 B61168  
 cocoonase (EC 3.4.21.-) - Chinese oak silkmoth (fragment)  
 C;Species: Antherea pernyi (Chinese oak silkmoth)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C;Accession: B61168  
 R;Kramer, K.J.; Pelsted, R.L.; Law, J.H.  
 J. Biol. Chem. 248, 3021-3028, 1973  
 A;Title: Cocoonase. V. Structural studies on an insect serine protease.  
 A;Reference number: A61168; MUID:73166540; PMID:4735570  
 A;Accession: B61168  
 A;Molecule type: protein  
 A;Residues: 1-5 <KRA>  
 C;Keywords: hydrolase; serine proteinase; zymogen  
 F;1-5/Product: cocoonase (fragment) #status experimental <MAT>

Query Match 40.0%; Score 10; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VG 3  
 ||  
 2 VG 3

RESULT 11  
 A44692  
 fulicin - giant African snail  
 C;Species: Achatina fulica (giant African snail)  
 C;Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
 C;Accession: A44692  
 R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No  
 Biochem. Biophys. Res. Commun. 178, 486-493, 1991  
 A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from b  
 A;Reference number: A44692; MUID:91315471; PMID:1859408  
 A;Accession: A44692  
 A;Molecule type: protein  
 A;Residues: 1-5 <OHT>  
 A;Cross-references: UNIPROT:P35905  
 C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide  
 F;2/Modified site: D-asparagine (Asn) #status experimental  
 F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 40.0%; Score 10; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FV 2  
 ||

Db 4 FV 5

RESULT 12  
 A32516  
 cholecystokinin-5 - dog  
 N;Alternate names: CCK-5  
 C;Species: Canis lupus familiaris (dog)  
 C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
 C;Accession: A32516  
 R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.  
 Am. J. Physiol. 252, G272-G275, 1987  
 A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest  
 A;Reference number: A32516; MUID:87153871; PMID:3826354  
 A;Accession: A32516  
 A;Molecule type: protein  
 A;Residues: 1-5 <SHI>  
 C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto  
 C;Superfamily: gastrin  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GLM 5  
 ||  
 1 GLM 3

RESULT 13  
 A58728  
 serrawettin W2 - Serratia marcescens  
 C;Species: Serratia marcescens  
 C;Date: 10-Feb-1998 #sequence\_revision 12-Feb-1998 #text\_change 12-Feb-1998  
 C;Accession: A58728  
 R;Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.  
 J. Bacteriol. 174, 1769-1776, 1992  
 A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and  
 A;Reference number: A58728; MUID:92193260; PMID:1548227  
 A;Accession: A58728  
 A;Status: unencoded polypeptide  
 A;Molecule type: protein  
 A;Residues: 1-5 <MAT>  
 A;Experimental source: strain NS 25  
 C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocatio  
 C;Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencode  
 F;1/Modified site: D-leucine (leu) #status experimental  
 F;4/Modified site: D-phenylalanine (Phe) #status experimental  
 F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status expe

Query Match 36.0%; Score 9; DB 4; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FV 2  
 ||  
 4 FI 5

Db 4 FI 5

RESULT 14  
 PT0633  
 T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C;Accession: PT0633  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0633  
 A;Status: translation not shown

A;Molecule type: mRNA  
A;Residues: 1-4 <FEE>  
A;Cross-references: UNIPROT:Q8BIV7  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 32.0%; Score 8; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
|:  
Db 3 GI 4

RESULT 15  
A44955  
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment  
C;Species: Vibrio harveyi  
C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 26-May-2000  
C;Accession: A44955  
R;Paquette, O.; Tu, S.C.  
Photochem. Photobiol. 50, 817-825, 1989  
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib  
A;Reference number: A44955; MUID:90175700; PMID:2628493  
A;Accession: A44955  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <PAQ>  
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 32.0%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GL 4  
|:  
Db 2 GI 3

Search completed: March 23, 2005, 14:51:54  
Job time : 24.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:21:29 ; Search time 112.5 Seconds  
(without alignments)  
22.759 Million cell updates/sec

Title: SR02  
Perfect score: 25  
Sequence: 1 fvglm 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 53

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	64.0	5	1 TPIS_CANFA	P54714 canis famil
2	10	40.0	4	1 EOSI_HUMAN	P02731 homo sapien
3	10	40.0	5	1 ALI4_CARMA	P81817 carcinus ma
4	10	40.0	5	1 EI03_LITRU	P82099 litoria rub
5	10	40.0	5	1 RE32_LITRU	P82073 litoria rub
6	10	40.0	5	1 UP01_MOUSE	P38639 mus musculu
7	9	36.0	4	1 ILME_SEPOP	P83568 sepia offic
8	9	36.0	5	1 EI04_LITRU	P82100 litoria rub
9	7	28.0	4	1 DCML_PSECH	P19916 pseudomonas
10	7	28.0	4	1 FLRF_HIRME	P42561 hirudo medi
11	7	28.0	4	1 FLRN_ATEL	P58707 anthopleura
12	7	28.0	4	1 FWRP_MACNI	P01162 macrocallis
13	6	24.0	2	1 GNA_SEPOP	P83570 sepia offic
14	6	24.0	3	1 GRWV_HUMAN	P01157 homo sapien
15	6	24.0	4	1 ACHI_ACHFU	P35904 achatina fu
16	6	24.0	4	1 FAR3_HIRME	P42562 hirudo medi
17	6	24.0	4	1 FAR4_HIRME	P42563 hirudo medi
18	6	24.0	4	1 FFAA_ATEL	P58705 anthopleura
19	6	24.0	4	1 FRII_ATEL	P58706 anthopleura
20	6	24.0	4	1 OCP1_OCTMI	P58648 octopus min
21	6	24.0	4	1 OCP3_OCTMI	P58649 octopus min
22	6	24.0	4	2 Q16047	Q16047 homo sapien
23	6	24.0	5	1 AP21_EISFO	P84182 eisenia foe
24	6	24.0	5	1 FARP_ARTTR	P41853 artiposthi
25	6	24.0	5	1 FARP_CHICK	P83308 gallus gall
26	6	24.0	5	1 PAP2_PARMA	P81864 pardachirus
27	6	24.0	5	1 PSK_DAUCA	P58261 daucus caro
28	6	24.0	5	1 RE11_LITRU	P82070 litoria rub
29	6	24.0	5	1 RE21_LITRU	P82071 litoria rub
30	6	24.0	5	1 RE31_LITRU	P82072 litoria rub
31	6	24.0	5	1 SUGA_ACHDO	P19991 acheta dome

32	6	24.0	5	1 UC22_MAIZE	P80628 zea mays (m
33	6	24.0	5	1 UXA4_CHLTR	P38005 chlamydia t
34	5	20.0	4	1 DCMS_PSECH	P19918 pseudomonas
35	5	20.0	4	2 Q96AT0	Q96AT0 homo sapien
36	5	20.0	5	1 BIOA_CITFR	P13071 citrobacter
37	5	20.0	5	1 BIOB_CITFR	P12997 citrobacter
38	5	20.0	5	2 Q99007	Q99007 hordeum vul
39	5	20.0	5	2 P83073	P83073 bacillus ce
40	4	16.0	4	1 YLM1_YEAST	P38515 saccharomyc
41	4	16.0	4	2 Q08433	Q08433 rattus sp.
42	4	16.0	5	1 PRCT_CARMA	P67857 carcinus ma
43	4	16.0	5	1 PRCT_LIMPO	P67858 limulus pol
44	4	16.0	5	1 PRCT_PERAM	P67859 periplaneta
45	3	12.0	3	1 LUXE_VIBFI	P24272 vibrio fisc

## ALIGNMENTS

RESULT 1  
TPIS\_CANFA STANDARD; PRT; 5 AA.  
ID TPIS\_CANFA  
AC P54714;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) (Fragment).  
GN Name=TP11;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
EX MEDLINE=98163340; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins";  
RL Electrophoresis 18:2795-2802(1997).  
CC -|- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone phosphate.  
CC -|- PATHWAY: Plays an important role in several metabolic pathways.  
CC -|- SUBUNIT: Homodimer (By similarity).  
CC -|- SIMILARITY: Belongs to the triosephosphate isomerase family.  
DR HSC-2DPAGE; P54714; DOG.  
DR InterPro; IPR000652; Triophos ismrse.  
DR PROSITE; PS00171; TIM; PARTIAL.  
KW Direct protein sequencing; Fatty acid biosynthesis; Gluconeogenesis; Glycolysis; Isomerase; Pentose shunt.  
FT NON TER 1  
FT NON TER 5  
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;  
Query Match 64.0%; Score 16; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FVG 3  
Db 1 FVG 3  
RESULT 2  
EOSI\_HUMAN STANDARD; PRT; 4 AA.  
ID EOSI\_HUMAN  
AC P02731;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bosinophilotoxic peptides.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76078412; PubMed=1060093;  
 RA Goetzl E.J., Austen K.F.;  
 RT "Purification and synthesis of eosinophilotoxic tetrapeptides of  
 RT human lung tissue: identification as eosinophil chemotactic factor of  
 RT anaphylaxis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -1- MISCELLANEOUS: These peptides are released from mast cells in lung  
 CC (and other tissues) during hypersensitivity reactions  
 CC (anaphylaxis). Their activities, preferentially affecting  
 CC eosinophils, include chemotaxis, chemotactic deactivation, release  
 CC of enzymes, and stimulation of the hexose monophosphate shunt.  
 DR GO; GO:0006935; P:chemotaxis; IDA.  
 DR GO; GO:0006955; P:immune response; IDA.  
 KW Direct protein sequencing.  
 FT VARIANT 1 1 V -> A (in other peptide).  
 FT /FTID=VAR\_005201.  
 SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;  
 Query Match 40.0%; Score 10; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VG 3  
 Db ||  
 1 VG 2

RESULT 3  
 AL14\_CARMA  
 ID AL14\_CARMA STANDARD; PRT; 5 AA.  
 AC P81817;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Carcinnatatin 14.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- SIMILARITY: May act as a neurotransmitter or neuromodulator.  
 CC -1- FUNCTION: Belongs to the allatostatin family.  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.  
 FT MOD\_RES 5 5 Leucine amide (Potential).  
 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;  
 Query Match 40.0%; Score 10; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GL 4  
 Db ||  
 4 GL 5

RESULT 4  
 EI03\_LITRU  
 ID EI03\_LITRU STANDARD; PRT; 5 AA.  
 AC P82039;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76078412; PubMed=1060093;  
 RA Goetzl E.J., Austen K.F.;  
 RT "Purification and synthesis of eosinophilotoxic tetrapeptides of  
 RT human lung tissue: identification as eosinophil chemotactic factor of  
 RT anaphylaxis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -1- MISCELLANEOUS: These peptides are released from mast cells in lung  
 CC (and other tissues) during hypersensitivity reactions  
 CC (anaphylaxis). Their activities, preferentially affecting  
 CC eosinophils, include chemotaxis, chemotactic deactivation, release  
 CC of enzymes, and stimulation of the hexose monophosphate shunt.  
 DR GO; GO:0006935; P:chemotaxis; IDA.  
 DR GO; GO:0006955; P:immune response; IDA.  
 KW Direct protein sequencing.  
 FT VARIANT 1 1 V -> A (in other peptide).  
 FT /FTID=VAR\_005201.  
 SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;  
 Query Match 40.0%; Score 10; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VG 3  
 Db ||  
 1 VG 2

RESULT 5  
 RE32\_LITRU  
 ID RE32\_LITRU STANDARD; PRT; 5 AA.  
 AC P82073;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Rubellidin 3.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
 OC Pelodyridae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing.  
 FT MOD\_RES 5 5 Methionine amide.  
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;  
 Query Match 40.0%; Score 10; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FV 2  
 Db ||  
 1 FV 2

RESULT 6  
 UF01\_MOUSE  
 ID UF01\_MOUSE STANDARD; PRT; 5 AA.  
 AC P38639;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
 OC Pelodyridae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide; Direct protein sequencing.  
 FT MOD\_RES 5 5  
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;  
 Query Match 40.0%; Score 10; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VG 3  
 Db ||  
 1 VG 2

```

DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; Wichter L.L., He C., Selkirk J.K.;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis."
RT Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON TER
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 40.0%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVG 3
Db 1 WIG 3

RESULT 7
ILME SEPOF
ID ILME SEPOF STANDARD; PRT; 4 AA.
AC P83568;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pheromone peptide ILME.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Egg;
RX MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;
RA Zatyiny C., Gagnon J., Boucaud-Cano E., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis."
RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
RN [2]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
RA Zatyiny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide."
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -1- FUNCTION: Has myotropic activity targeting the genital tract.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg(EC2).
CC -1- MASS SPECTROMETRY: MW=505.4; METHOD=NALDI; RANGE=1-4; NOTE=Ref.1.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 36.0%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LM 5
Db 11

```

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Db 2 LM 3

RESULT 8
EIO4 LITRU
ID EIO4 LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 36.0%; Score 9; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FV 2
Db 1 FI 2

RESULT 9
DCWL PSECH
ID DCWL PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17; Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN Name=cutL;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of Co dehydrogenase structural genes in
RT carboxydohydrogenic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -1- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1
CC molybdopterin cytosine dinucleotide (MCD) per subunit.
CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
DR PIR; P10140; P10140.
KW Direct protein sequencing; Molybdenum; Oxidoreductase.
FT NON TER
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;

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Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VG 3  
:|  
Db 1 MG 2

RESULT 10  
FLRN\_HIRME STANDARD; PRT; 4 AA.  
ID FLRN\_HIRME  
AC P42561;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE FLRFamide.  
OS Hirudo medicinalis (Medicinal leech), and  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudines;  
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=6421, 27815;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=H. medicinalis;  
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of RFamide neuropeptides in the medicinal leech.";  
RL Peptides 12:897-908(1991).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=H. trivolvis; TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRamide-related peptides from the kidney of the snail, Helisoma trivolvis";  
RL Peptides 15:31-36(1994).  
RN [3]  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 582 MW; 6940729A0000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FV 2  
:|  
Db 1 FL 2

RESULT 11  
FLRN\_ANTEL STANDARD; PRT; 4 AA.  
ID FLRN\_ANTEL  
AC P58707;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Anthopleura elegantissima (Sea anemone).  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Anthopleura elegantissima (Sea anemone).  
RX MEDLINE=90319122; PubMed=1973541;  
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
RA Reinscheid R.K., Nethacker H.-P., Staley A.L.;  
RT "Isolation of L-3-phenylalanyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea anemone neuropeptide containing an unusual amino-terminal blocking group";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).

CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Neuron specific.  
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGS=1-4; NOTE=Ref.1.  
DR PIR: A35779; A35779.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 1 1 3-phenyllactic acid.  
FT MOD RES 4 4 Asparagine amide.  
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FV 2  
:|  
Db 1 FL 2

RESULT 12  
FMRF\_MACNI STANDARD; PRT; 4 AA.  
ID FMRF\_MACNI  
AC P01162;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE FMRamide (Peak C) (Cardioexcitatory neuropeptide).  
OS Macrocallista nimbosa (Sun-ray clam),  
OS Nereis virens (Sandworm),  
OS Hirudo medicinalis (Medicinal leech), and  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
OC Veneroidea; Veneridae; Macrocallista.  
OX NCBI\_TaxID=6594, 6353, 6421, 27815;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC SPECIES=M. nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;  
RX MEDLINE=77215956; PubMed=877582;  
RA Price D.A., Greenberg M.J.;  
RT "Structure of a molluscan cardioexcitatory neuropeptide";  
RL Science 197:670-671(1977).  
RN [2]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC SPECIES=M. nimbosa; TISSUE=Ganglion;  
RX MEDLINE=78012038; PubMed=909875;  
RA Price D.A., Greenberg M.J.;  
RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc";  
RL Prep. Biochem. 7:261-281(1977).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=N. virens;  
RX MEDLINE=90259866; PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;  
RA Krajniak K.G., Price D.A.;  
RT "Authentic FMRamide is present in the polychaete Nereis virens.";  
RL Peptides 11:75-77(1990).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=H. medicinalis;  
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of RFamide neuropeptides in the medicinal leech.";  
RL Peptides 12:897-908(1991).  
RN [5]  
RP SEQUENCE.  
RC SPECIES=H. trivolvis; TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRamide-related peptides from the kidney of the snail, Helisoma trivolvis";  
RL Peptides 15:31-36(1994).  
RN [6]  
CC -1- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of cardiac contraction.



CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the PARP (FMRamide related peptide)  
 CC family.  
 DR PIR; A01426; BCNK.  
 DR PIR; A60418; A60418.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 4 4 Phenylalanine amide.  
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FV 2  
 Db 1 FM 2

RESULT 13  
 GWA\_SEPOF STANDARD; PRT; 2 AA.  
 AC P83570;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide Gwa.  
 OS Sepia officinalis (Common cuttlefish).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
 OX NCBI\_TaxID=6610;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Optic lobe;  
 RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;  
 RA Henry J., Favrel P., Boucaud-Camou E.;  
 FT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
 RT peptide inhibiting the motility of the mature oviduct in the  
 RL cuttlefish, Sepia officinalis";  
 RL Peptides 18:1469-1474(1997).  
 CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity  
 CC targeting the distal oviduct. Inhibits the motility of the oviduct  
 CC by decreasing tonus, frequency and amplitude of contractions.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=WALDI; RANGE=1-2; NOTE=Ref.1.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 2 2 Tryptophan amide.  
 SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 G 3  
 Db 1 G 1

RESULT 14  
 GRWM\_HUMAN STANDARD; PRT; 3 AA.  
 AC P01157;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Growth-modulating peptide.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77162369; PubMed=858356;  
 RA Schlesinger D.H., Pickart L., Thaler M.M.;

RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
 RL Experientia 33:324-325(1977)  
 CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
 CC growth of some cell types and to inhibit other types in vitro.  
 DR GO; GO:0001558; P:regulation of cell growth; NAS.  
 KW Direct protein sequencing.  
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 G 3  
 Db 1 G 1

RESULT 15  
 ACHI\_ACHF STANDARD; PRT; 4 AA.  
 ID ACHI\_ACHF  
 AC P35904;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Achatin-I.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN=Perussac; TISSUE=Ganglion;  
 RX MEDLINE=89273551; PubMed=2597281;  
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica Perussac containing a D-amino acid residue.";  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=Perussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;  
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Munsoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function.";  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]  
 RP CRYSTALLIZATION.  
 RX MEDLINE=93014529; PubMed=1399265;  
 RA Iwashita T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
 RT Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid  
 RT residue.";  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
 CC and produces a spike broadening of the identified heart excitatory  
 CC neuron (PON); also enhances the amplitude and frequency of the  
 CC heart beat. Has also an effect on several other muscles.  
 DR PIR; A32480; A32480.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD\_RES 2 2 D-phenylalanine.  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 G 3  
 Db 1 G 1

Search completed: March 23, 2005, 14:49:56  
Job time : 112.5 secs

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Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	25	100.0	5	4	AAB82430	Fluorinat
2	25	100.0	5	4	AAB82431	Fluorinat
3	20	80.0	5	2	AAR33009	Alpha-sub
4	20	80.0	5	2	AAR33008	Alpha-sub
5	20	80.0	5	2	AAR33007	Alpha-sub
6	20	80.0	5	2	AAR33010	Alpha-sub
7	20	80.0	5	2	AAR80134	COOH-term
8	20	80.0	5	2	AAR54549	Cholecyst
9	20	80.0	5	2	AAR54551	Cholecyst
10	20	80.0	5	2	AAR54550	Cholecyst
11	20	80.0	5	2	AAR54548	Cholecyst
12	20	80.0	5	2	AAW41687	Tetrapept
13	20	80.0	5	2	AAW99643	Substance
14	20	80.0	5	2	AAW50325	Neutroph
15	20	80.0	5	2	AAW92660	Human tac
16	20	80.0	5	3	AAB23028	Mammalian
17	20	80.0	5	3	AAB23025	Human/rat
18	20	80.0	5	3	AAW67576	P antagon
19	20	80.0	5	4	AAB66674	C-termina
20	20	80.0	5	4	AAB91428	Tachykini
21	20	80.0	5	4	AAB70556	Octopus t
22	20	80.0	5	5	AAU10880	Human bet
23	20	80.0	5	5	ABB10088	Substance
24	20	80.0	5	5	AUU77847	Tachykini
25	20	80.0	5	5	AAU77845	Tachykini

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XX PS Example 3; Col 20; 25pp; English.
XX CC The present sequence is that of a protected peptide produced as an
XX CC intermediate in the chemical synthesis of a novel fluorinated neurokinin
XX CC A antagonist (AAB82428). Fluorinated neurokinin A antagonists of the
XX CC invention are based on the amino acid sequence of neurokinin A, but
XX CC include at least 1 modified peptide bond having a reduced amide and a
XX CC fluorinated alkyl attached to the N atom of the modified peptide bond.
XX CC The neurokinin A antagonists are useful as immunosuppressives and in
XX CC treating subjects, including humans, with various conditions, e.g. asthma
XX CC (claimed), arthritis, urinary incontinence, pain, inflammation, tumour
XX CC growth, gastrointestinal hypermotility, Huntington's disease, psychosis,
XX CC neuritis, neuralgia, urticaria, carcinoma, carcinoid syndrome symptoms, influenza,
XX CC common cold, and headache including migraine
XX SQ Sequence 5 AA;
      Query Match      100.0%; Score 25; DB 4; Length 5;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVGLM 5
Db 1 FVGLM 5

RESULT 2
AAB82431
ID AAB82431 standard; peptide; 5 AA.
XX AC AAB82431;
XX DT 22-AUG-2001 (first entry)
XX DE Fluorinated neurokinin A antagonist intermediate.
XX KW Neurokinin A; fluorinated peptide; antagonist; immunosuppressive;
XX KW antiarthritic; antiaachmatic; antiinflammatory; antiarthritic; analgesic;
XX KW antitumour; anticonvulsant; nootropic; antipsychotic; antimigraine;
XX KW asthma; therapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1..2
XX FT Modified-site /note= "the peptide bond is replaced by CH2-N(CH2CF3)"
XX FT Modified-site 5
XX FT Modified-site /note= "C-terminal amide"
XX PN US6218364-B1.
XX PD 17-APR-2001.
XX PF 26-APR-1996; 96US-00638407.
XX PR 20-JUN-1988; 88US-00208926.
XX PR 24-FEB-1989; 89US-00315202.
XX PR 23-MAY-1989; 89US-00356031.
XX PR 17-APR-1991; 91US-00686593.
XX PR 31-MAY-1991; 91US-00709092.
XX PR 19-MAR-1993; 93US-00033987.
XX PR 29-JUL-1994; 94US-00282341.
XX XX (HARB/) HARBESON S L.
XX PA (MCCA/) MCCARTHY J R.
XX XX Harbeson SL, McCarthy JR;
XX DR WPI; 2001-366135/38.
XX PT New peptide derivative useful as immunosuppressants and in treating
XX PT subjects with various conditions, e.g. asthma.

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XX PS Example 3; Col 20; 25pp; English.
XX CC The present sequence is that of a synthetic peptide produced as an
XX CC intermediate in the chemical synthesis of a novel fluorinated neurokinin
XX CC A antagonist (AAB82428). Fluorinated neurokinin A antagonists of the
XX CC invention are based on the amino acid sequence of neurokinin A, but
XX CC include at least 1 modified peptide bond having a reduced amide and a
XX CC fluorinated alkyl attached to the N atom of the modified peptide bond.
XX CC The neurokinin A antagonists are useful as immunosuppressives and in
XX CC treating subjects, including humans, with various conditions, e.g. asthma
XX CC (claimed), arthritis, urinary incontinence, pain, inflammation, tumour
XX CC growth, gastrointestinal hypermotility, Huntington's disease, psychosis,
XX CC neuritis, neuralgia, urticaria, carcinoma, carcinoid syndrome symptoms, influenza,
XX CC common cold, and headache including migraine
XX SQ Sequence 5 AA;
      Query Match      100.0%; Score 25; DB 4; Length 5;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVGLM 5
Db 1 FVGLM 5

RESULT 3
AAR33009
ID AAR33009 standard; peptide; 5 AA.
XX AC AAR33009;
XX DT 25-MAR-2003 (revised)
XX DT 02-APR-1993 (first entry)
XX DE Alpha-substituted short peptide.
XX KW CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
XX KW improved bioavailability.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 4
XX FT Modified-site /note= "alpha-Me-Leu"
XX FT Modified-site 5
XX FT Modified-site /note= "Met-NH2"
XX PN WO9219254-A1.
XX PD 12-NOV-1992.
XX PF 15-APR-1992; 92WO-US003119.
XX PR 24-APR-1991; 91US-00690755.
XX PR 20-MAR-1992; 92US-00852086.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Horwell DC, Hughes J, Richardson RS, Howson W;
XX DR WPI; 1992-398522/48.
XX XX New alpha-substd. polypeptide are e.g. selective receptor ligands - for
XX PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
XX PT depression, cancer, asthma, psychosis, arthritis, etc.
XX PS Claim 3; Page 41; 46pp; English.
XX CC The peptide is a specifically claimed example of a group of generically
XX CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
XX CC substituent on an alpha-C atom in the chain. Such substitution may modify

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CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptive. (Updated on 25-MAR-2003 to correct PI field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 |  
 |  
 |  
 |  
 Db 1 FVGLM 5

RESULT 4

AAR33008  
 ID AAR33008 standard; peptide; 5 AA.

XX AC AAR33008;

XX 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

DE CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
 KW improved bioavailability.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 2

FT Modified-site 5 /note= "alpha-Me-Phe"

FT Modified-site 5 /note= "Met-NH2"

XX WO9219254-A1.

XX 12-NOV-1992.

XX 15-APR-1992; 92WO-US003119.

XX 24-APR-1991; 91US-00690755.

PR 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.

XX Horwell DC, Hughes J, Richardson RS, Howson W;

XX WPI; 1992-398522/48.

XX New alpha-subst. polypeptide are e.g. selective receptor ligands - for  
 PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
 PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
 CC substituent on an alpha-C atom in the chain. Such substitution may modify  
 CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating

CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptive. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 |  
 |  
 |  
 |  
 Db 1 FVGLM 5

RESULT 5

AAR33007  
 ID AAR33007 standard; peptide; 5 AA.

XX AC AAR33007;

XX 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

DE CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
 KW improved bioavailability.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT Modified-site 5 /note= "alpha-Me-Phe"

FT Modified-site 5 /note= "Met-NH2"

XX WO9219254-A1.

XX 12-NOV-1992.

XX 15-APR-1992; 92WO-US003119.

XX 24-APR-1991; 91US-00690755.

PR 20-MAR-1992; 92US-00852086.

XX (WARN ) WARNER LAMBERT CO.

XX Horwell DC, Hughes J, Richardson RS, Howson W;

XX WPI; 1992-398522/48.

XX New alpha-subst. polypeptide are e.g. selective receptor ligands - for  
 PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
 PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
 CC substituent on an alpha-C atom in the chain. Such substitution may modify  
 CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure, cancer,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as

CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 Db 1 FVGLM 5

RESULT 6  
 AAR33010  
 ID AAR33010 standard; peptide; 5 AA.

XX AAR33010;

AC 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;  
 KW improved bioavailability.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 5  
 FT /note= "alpha-Me-Met-NH2"

XX WO9219254-A1.

XX 12-NOV-1992.

XX 15-APR-1992; 92WO-US003119.

XX 24-APR-1991; 91US-00690755.

XX 20-MAR-1992; 92US-00852086.

XX (WARN) WARNER LAMBERT CO.

XX Horwell DC, Hughes J, Richardson RS, Howson W;

XX WPI; 1992-398522/48.

XX New alpha-substd. polypeptide are e.g. selective receptor ligands - for  
 PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,  
 PT depression, cancer, asthma, psychosis, arthritis, etc.

XX Claim 3; Page 41; 46pp; English.

XX The peptide is a specifically claimed example of a group of generically  
 CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a  
 CC substituent on an alpha-C atom in the chain. Such substitution may modify  
 CC the bioavailability, stability or absorbability of the peptide and hence  
 CC may improve the activity of the peptide as a drug. Depending on the  
 CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic  
 CC peptide, etc.), the modified peptides are variously useful for treating  
 CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,  
 CC addictive drug withdrawal symptoms, hypertension, heart failure, cancer,  
 CC cognition or memory disorders, spasticity, depression, diabetes, cancer,  
 CC asthma, bladder dysfunction, psychosis and arthritis; and as  
 CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on  
 CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 Db 1 FVGLM 5

RESULT 7

AAW80134

ID AAW80134 standard; peptide; 5 AA.

XX AAW80134;

XX 17-DEC-1998 (first entry)

XX COOH-terminal sequence of the tachykinin family.

XX Human; neurokinin receptor; NK-2; neurokinin A neurotransmitter;  
 KW abnormal smooth muscle cell contraction; asthma; PCR primer;  
 KW gastrointestinal disorder; peptic ulcer; ulcerative colitis.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 2  
 FT /note= "Phe, Tyr, Val or Ile"

XX WO9216220-A1.

XX 01-OCT-1992.

XX 13-MAR-1992; 92WO-US002017.

XX 15-MAR-1991; 91US-00670066.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Gerard NP, Gerard C;

XX WPI; 1992-348932/42.

XX Human recombinant neurokinin NK-2 receptor - antagonises interaction of  
 PT neurokinin A and its receptor, useful for treating asthma and ulcerative  
 PT colitis, etc.

XX Disclosure; Page 1; 43pp; English.

XX The present sequence represents the COOH-terminal sequence of the  
 CC tachykinin family. The specification describes a human recombinant  
 CC neurokinin (NK-2) receptor protein. The human NK-2 receptor gene was  
 CC cloned from human tracheal tissue from an individual with cystic  
 CC fibrosis. The coding sequence is interrupted by four introns. The protein  
 CC can be used to screen for compounds that antagonise the interaction  
 CC between neurokinin A neurotransmitter and its NK-2 receptor. The protein  
 CC is thus useful for treating disorders associated with abnormal smooth  
 CC muscle cell contraction, particularly asthma and gastrointestinal  
 CC disorders such as peptic ulcers and ulcerative colitis

XX Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 Db 1 FVGLM 5

RESULT 8

AAW54549

KW	Gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW	heart failure; cognition; memory enhancement; spasticity; depression;
KW	diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 5
FT	/label= MeMet
FT	/note= "Amidated C-terminal"
XX	
PN	W09409031-A1.
XX	
PD	28-APR-1994.
XX	
PP	14-OCT-1993; 93WO-US009809.
XX	
PR	19-OCT-1992; 92US-00963169.
PR	08-OCT-1993; 93US-00131693.
XX	
PA	(WARN ) WARNER LAMBERT CO.
XX	
PI	Horwell DC, Howson W, Hugues J, Richardson RS;
XX	
DR	WPI; 1994-151243/18.
XX	
PT	New cholecystokinin analogues - useful e.g. in treatment of pain,
PT	obesity, stroke, anxiety, and gastrointestinal ulcers.
XX	
PS	Claim 3; Page 66; 73pp; English.
XX	
CC	The sequences given in AAR53117-38 and AAR54530-51 are peptide analogues
CC	of cholecystokinin (CCK) which can be used to treat obesity, anxiety,
CC	Gastrointestinal ulcers, pain, stroke, inflammation, hypertension, heart
CC	failure, cognition, memory enhancement, spasticity, depression, diabetes,
CC	cancers, asthma, bladder dysfunction, psychosis, arthritis and in the
CC	treatment of substance withdrawal. (Updated on 25-MAR-2003 to correct PN
CC	field.)
XX	
SQ	Sequence 5 AA;
	Query Match 80.0%; Score 20; DB 2; Length 5;
	Best Local Similarity 80.0%; Pred. No. 1.8e+06;
	Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 FVGLM 5
DB	1 FFGLM 5
	RESULT 10
AAR54550	
ID	AAR54550 standard; peptide, 5 AA.
XX	
AC	AAR54550;
XX	
DT	25-MAR-2003 (revised)
DT	14-DEC-1994 (first entry)
XX	
DE	Cholecystokinin analogue peptide #43.
XX	
KW	Peptide analogue; peptoid; cholecystokinin; CCK; obesity; anxiety;
KW	Gastrointestinal ulcers; pain; stroke; inflammation; hypertension;
KW	heart failure; cognition; memory enhancement; spasticity; depression;
KW	diabetes; cancers; asthma; bladder dysfunction; psychosis; arthritis.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 3
FT	/label= MeLeu
FT	Modified-site 5
FT	/note= "Amidated C-terminal"





CC disorders such as corneal ulcer, corneal epithelial peeling, dry eye and  
 CC keratitis. The dosage is 0.1-5000 (preferably 1-1000) mg/day of the  
 CC active ingredient and 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The  
 CC preferable form of the composition is eye drops

XX Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 | | | |  
 DB 1 FGLM 5

#### RESULT 13

AAW99643  
 ID AAW99643 standard; peptide; 5 AA.

XX AAW99643;

AC AAW99643;

DT 21-MAY-1999 (first entry)

DE Substance P analogue peptide.

XX Substance P; myoblast transfer therapy; pain relief; analgesic;  
 KW behavioural abnormality; perceptible abnormality; opioid receptor;  
 KW psychiatric condition; depression; chronic anxiety syndrome; paranoia;  
 KW alcoholism; drug addiction; chronic pain; neuron.

XX Homo sapiens.

OS Synthetic.

XX EP898967-A1.

XX 03-MAR-1999.

PD 07-APR-1998; 98EP-00201068.

PF 11-AUG-1997; 97US-0055199P.

PR (CELL-) CELL THERAPY RES FOUND.

XX Law PK;

XX WPI; 1999-144555/13.

XX New composition for supplying peptide to opioid receptor - comprises  
 PT myogenic cells containing heterologous DNA encoding peptide and carrier.

PS Claim 8; Page 8; 11pp; English.

XX A composition has been developed for supplying a peptide to an opioid  
 CC receptor or that interferes with binding of substance P to its receptor.  
 CC The composition comprises: (a) myogenic cells that contain heterologous  
 CC DNA encoding the peptide to express the peptide; and (b) a  
 CC pharmacologically acceptable carrier. The composition is useful for  
 CC relieving pain and for treating behavioural and perceptible abnormalities  
 CC using myoblast transfer therapy. It is useful in a method for treating  
 CC psychiatric conditions that involve abnormal perception e.g. depression,  
 CC chronic anxiety syndromes, paranoia, alcoholism and drug addiction,  
 CC chronic pain and other diseases in which opioid neurons and substance P  
 CC sensitive neurons play a role. The composition provides a continuous,  
 CC long term supply of opioid peptides (long-term analgesia) which lasts for  
 CC up to at least 6 years. The present sequence represents a specifically  
 CC claimed substance P analogue

XX Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 | | | |  
 DB 1 FGLM 5

#### RESULT 14

AAAY50325  
 ID AAAY50325 standard; peptide; 5 AA.

XX AAAY50325;

XX 12-JAN-2000 (first entry)

DE Neutrophil-activating pancreatic derived peptide 125.

XX Cell activation; pancreas; treatment; cardiovascular disease; trauma;  
 KW inflammatory disease; autoimmune diseases; arthritis; diabetes; stroke;  
 KW organ rejection; ischemia; Alzheimer's disease; myocardial infarction;  
 KW haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina;  
 KW trauma; protease inhibitor; hypertension; sepsis.

XX Unidentified.

XX WO9946367-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99WO-US005247.

XX 11-MAR-1998; 98US-00038894.

XX (CELL-) CELL ACTIVATION INC.

XX (REGC) UNIV CALIFORNIA.

XX (SCRI) SCRIPPS RES INST.

XX Stoughton RB, Schmid-Schonbein GW, Hugli TE, Kistler E;

XX WPI; 1999-580234/49.

XX Use of cell activating compositions in developing products for diagnosis  
 CC and treatment of e.g. cardiovascular, inflammatory, autoimmune or  
 CC Alzheimer's disease, trauma, arthritis, organ rejection, diabetes, stroke  
 CC or ischemia.

XX Example 9; Page 184; 184pp; English.

XX This invention describes a novel method for the use and preparation of  
 CC cell activating compositions which involves preparing a cell activating  
 CC composition comprising (a) homogenizing pancreatic tissue in buffer at  
 CC about neutral or higher pH to produce a homogenate; (b) removing  
 CC particulates from the homogenate; (c) optionally incubating the resulting  
 CC homogenate, with particulates removed, with a protease; and (d)  
 CC fractionating the homogenate and selecting fractions that exhibit cell  
 CC activation activity. The methods can be used for improving treatment  
 CC outcome or reducing risk of treatment of e.g. cardiovascular disease,  
 CC inflammatory disease, trauma, autoimmune diseases, arthritis, organ  
 CC rejection, diabetes and diabetic complications, stroke, ischemia,  
 CC Alzheimer's disease, myocardial infarction, haemorrhagic shock, diabetic  
 CC retinopathy, diabetes, venous insufficiency, unstable angina or trauma.  
 CC They can be used in the veterinary treatment of a non-human subject.  
 CC Protease inhibitors can be used to lower cell activation resulting from  
 CC these diseases and deficiencies. The detection of an elevated level of  
 CC hydrogen peroxide can be used to detect an inflammatory condition. An  
 CC elevated level of hydrogen peroxide in plasma or whole blood and in the  
 CC presence of superoxide dismutase (SOD) indicates leukocyte up regulation,  
 CC e.g. indicative of the onset of an acute cardiovascular disorder, such  
 CC as disease onset or ischemic complications. An elevated level of hydrogen  
 CC peroxide in plasma or whole blood and a low level in the presence of SOD  
 CC is indicative of a chronic or immune compromised condition e.g.  
 CC hypertension or sepsis. AAAY50201-150334 represent peptides used in the  
 CC method of the invention

XX

SQ Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5  
 |  
 |  
 |  
 |  
 Db 1 PFGLM 5

RESULT 15

AAW92660

ID AAW92660 standard; peptide; 5 AA.

XX

AC AAW92660;

XX

DT 20-MAR-2003 (revised)

DT 30-APR-1999 (first entry)

XX

DE Human tachykinin agonist beta-amyloid peptide fragment #6.

XX

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.

XX

OS Homo sapiens.

XX

FN US5876948-A.

XX

PD 02-MAR-1999.

XX

PF 29-JUL-1991; 91US-00737371.

XX

PR 27-JUL-1990; 90US-00559173.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX

PI Yankner BA;

XX

DR WPI; 1999-189630/16.

XX

PT Screening for neurotoxin inhibitors - by testing compounds for their

effect on beta-amyloid peptide neurotoxic effect on neuronal cells.

XX

PS Disclosure; Col 13-14; 28pp; English.

XX

CC This invention describes a method for screening compounds for inhibiting  
 a neurotoxin. The method involves incubating tachykinin agonists with  
 neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be  
 used for identifying compounds for treating diseases characterised by an  
 undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,  
 Down's syndrome, and the syndromes of hereditary cerebral haemorrhage  
 with amyloidosis and non-inherited congophilic angiopathy with cerebral  
 haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human  
 beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF  
 field.)

XX

SQ Sequence 5 AA;

Query Match 80.0%; Score 20; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5  
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 |  
 |  
 |  
 Db 1 PFGLM 5

Search completed: March 23, 2005, 14:46:01  
 Job time : 121.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:50:07 ; Search time 92 Seconds  
(without alignments)  
17.995 Million cell updates/sec

Title: SEQ2  
Perfect score: 25  
Sequence: 1 fvglm 5

Scoring table: BLOSUM62  
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Searched: 1407402 seqs, 311100923 residues

Total number of hits satisfying chosen parameters: 21937

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	20	80.0	5	9	US-09-265-690C-1
2	20	80.0	5	9	US-09-265-690C-4
3	20	80.0	5	14	US-10-230-133-4
4	20	80.0	5	14	US-10-053-669-1
5	20	80.0	5	14	US-10-053-669-4
6	20	80.0	5	15	US-10-134-187-3
7	20	80.0	5	16	US-10-688-741-3
8	20	80.0	5	16	US-10-695-536-4
9	20	80.0	5	16	US-10-805-881-1
10	20	80.0	5	16	US-10-805-881-4
11	20	80.0	5	17	US-10-497-628-15
12	17	68.0	5	14	US-10-168-789A-32
13	17	68.0	5	17	US-10-497-628-16

14	16	64.0	4	8	US-08-484-409-30	Sequence 30, Appl
15	16	64.0	4	13	US-10-033-026-2	Sequence 2, Appl
16	16	64.0	5	10	US-09-992-124A-14	Sequence 14, Appl
17	16	64.0	5	14	US-10-168-789A-39	Sequence 39, Appl
18	16	64.0	5	17	US-10-641-286-27	Sequence 27, Appl
19	15	60.0	3	14	US-10-230-133-2	Sequence 2, Appl
20	15	60.0	3	16	US-10-695-536-2	Sequence 2, Appl
21	15	60.0	4	9	US-09-265-690C-2	Sequence 2, Appl
22	15	60.0	4	14	US-10-230-133-3	Sequence 3, Appl
23	15	60.0	4	14	US-10-053-669-2	Sequence 2, Appl
24	15	60.0	4	16	US-10-695-536-3	Sequence 3, Appl
25	15	60.0	4	16	US-10-805-881-2	Sequence 2, Appl
26	15	60.0	4	17	US-10-497-628-2	Sequence 2, Appl
27	15	60.0	4	17	US-10-821-240A-270	Sequence 270, App
28	15	60.0	5	10	US-09-992-124A-5	Sequence 5, Appl
29	15	60.0	5	15	US-10-243-613-79	Sequence 79, Appl
30	15	60.0	5	16	US-10-128-520-360	Sequence 360, App
31	15	60.0	5	16	US-10-346-737A-30	Sequence 30, Appl
32	15	60.0	5	17	US-10-497-628-17	Sequence 17, Appl
33	15	60.0	5	17	US-10-641-286-13	Sequence 13, Appl
34	14	56.0	4	9	US-09-943-123-24	Sequence 24, Appl
35	14	56.0	4	14	US-10-087-402-10	Sequence 10, Appl
36	14	56.0	4	14	US-10-361-290-12	Sequence 12, Appl
37	14	56.0	4	17	US-10-712-359A-24	Sequence 24, Appl
38	14	56.0	4	17	US-10-821-240A-244	Sequence 244, App
39	14	56.0	5	13	US-10-014-716-28	Sequence 28, Appl
40	14	56.0	5	14	US-10-190-951-28	Sequence 28, Appl
41	14	56.0	5	14	US-10-190-082-680	Sequence 680, App
42	14	56.0	5	15	US-10-299-867-67	Sequence 67, Appl
43	14	56.0	5	15	US-10-454-566-10	Sequence 10, Appl
44	14	56.0	5	15	US-10-436-549-565	Sequence 565, App
45	14	56.0	5	16	US-10-712-425-565	Sequence 565, App

#### ALIGNMENTS

RESULT 1  
US-09-265-690C-1  
; Sequence 1, Application US/09265690C  
; Publication No. US20010051345A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound M  
; FILE OF INVENTION: for Disease Diagnosis  
; FILE REFERENCE: 1427001  
; CURRENT APPLICATION NUMBER: US/09/265,690C  
; CURRENT FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: AMIDATION  
US-09-265-690C-1

Query Match 80.0%; Score 20; DB 9; Length 5;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
| | | |  
DB 1 FVGLM 5

RESULT 2  
US-09-265-690C-4  
; Sequence 4, Application US/09265690C  
; Publication No. US20010051345A1

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; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
; NAME/KEY: VARIANT
; LOCATION: (2)..(2)
; OTHER INFORMATION: "X" may be either Phe or Val.
US-09-265-690C-4

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Query Match      80.0%; Score 20; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 FVGLM 5
      ||||
Db      1 FXGLM 5

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RESULT 3
US-10-230-133-4
; Sequence 4, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
; NAME/KEY: VARIANT
; LOCATION: (2)..(2)
; OTHER INFORMATION: "X" may be either F or V.
US-10-230-133-4

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Query Match      80.0%; Score 20; DB 14; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 FVGLM 5
      ||||
Db      1 FXGLM 5

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RESULT 4
US-10-053-669-1
; Sequence 1, Application US/10053669
; Publication No. US20030077658A1

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; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound M
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
; OTHER INFORMATION: "X" may be either Phe or Val.
US-10-053-669-1

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Query Match      80.0%; Score 20; DB 14; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 FVGLM 5
      ||||
Db      1 FXGLM 5

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RESULT 5
US-10-053-669-4
; Sequence 4, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound M
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
; NAME/KEY: VARIANT
; LOCATION: (2)..(2)
; OTHER INFORMATION: "X" may be either Phe or Val.
US-10-053-669-4

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```

Query Match      80.0%; Score 20; DB 14; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 FVGLM 5
      ||||
Db      1 FXGLM 5

```

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RESULT 6
US-10-134-187-3
; Sequence 3, Application US/10134187
; Publication No. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.

```

; APPLICANT: Kream, Richard M.  
 ; APPLICANT: Kream, Richard M.  
 ; TITLE OF INVENTION: Chimeric Hybrid Analgesics  
 ; FILE REFERENCE: Kream  
 ; CURRENT APPLICATION NUMBER: US/10/134,187  
 ; CURRENT FILING DATE: 2002-04-26  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: mammalian  
 US-10-134-187-3

Query Match 80.0%; Score 20; DB 15; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5  
 Db 1 FFGLM 5

RESULT 7  
 US-10-688-741-3  
 ; Sequence 3, Application US/10688741  
 ; Publication No. US20040106636A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kream, Richard M.  
 ; APPLICANT: Kream, Richard M.  
 ; APPLICANT: Kream, Richard M.  
 ; TITLE OF INVENTION: Method Of Inhibiting Opioid Tolerance Development With Chimeric H  
 ; TITLE OF INVENTION: Analgesics  
 ; FILE REFERENCE: Kream  
 ; CURRENT APPLICATION NUMBER: US/10/688,741  
 ; CURRENT FILING DATE: 2003-10-17  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: mammalian  
 US-10-688-741-3

Query Match 80.0%; Score 20; DB 16; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5  
 Db 1 FFGLM 5

RESULT 8  
 US-10-695-536-4  
 ; Sequence 4, Application US/10695536  
 ; Publication No. US20040110692A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wells, Ibert Clifton  
 ; TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents  
 ; TITLE OF INVENTION: and Methods for Treatment of Abnormal Physiological States  
 ; FILE REFERENCE: 800812-0008  
 ; CURRENT APPLICATION NUMBER: US/10/695,536  
 ; CURRENT FILING DATE: 2003-10-28  
 ; PRIOR APPLICATION NUMBER: US 10/230,133  
 ; PRIOR FILING DATE: 2002-08-29  
 ; PRIOR APPLICATION NUMBER: US 09/635,266  
 ; PRIOR FILING DATE: 2000-08-09  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 4  
 ; LENGTH: 5  
 ; TYPE: PRT

; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: MISC FEATURE  
 ; LOCATION: (2)..(2)  
 ; OTHER INFORMATION: X can be either F or V  
 ; FEATURE:  
 ; NAME/KEY: MOD\_RES  
 ; LOCATION: (5)..(5)  
 ; OTHER INFORMATION: AMIDATION  
 US-10-695-536-4

Query Match 80.0%; Score 20; DB 16; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5  
 Db 1 FFGLM 5

RESULT 9  
 US-10-805-881-1  
 ; Sequence 1, Application US/10805881  
 ; Publication No. US20040171093A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wells, Ibert C.  
 ; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound  
 ; TITLE OF INVENTION: Magnesium for Disease Diagnosis  
 ; FILE REFERENCE: 800812-0005  
 ; CURRENT APPLICATION NUMBER: US/10/805,881  
 ; CURRENT FILING DATE: 2004-03-22  
 ; PRIOR APPLICATION NUMBER: US 10/053,669  
 ; PRIOR FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: US 10/695,536  
 ; PRIOR FILING DATE: 2003-10-28  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: MOD\_RES  
 ; LOCATION: (5)..(5)  
 ; OTHER INFORMATION: AMIDATION  
 US-10-805-881-1

Query Match 80.0%; Score 20; DB 16; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5  
 Db 1 FFGLM 5

RESULT 10  
 US-10-805-881-4  
 ; Sequence 4, Application US/10805881  
 ; Publication No. US20040171093A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wells, Ibert C.  
 ; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound  
 ; TITLE OF INVENTION: Magnesium for Disease Diagnosis  
 ; FILE REFERENCE: 800812-0005  
 ; CURRENT APPLICATION NUMBER: US/10/805,881  
 ; CURRENT FILING DATE: 2004-03-22  
 ; PRIOR APPLICATION NUMBER: US 10/053,669  
 ; PRIOR FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: US 10/695,536  
 ; PRIOR FILING DATE: 2003-10-28  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)..(2)
; OTHER INFORMATION: "X" may be either F or V
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-10-805-881-4

Query Match      80.0%; Score 20; DB 16; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5
Db 1 FXGLM 5

RESULT 11
US-10-497-628-15
; Sequence 15, Application US/10497628
; Publication No. US2005009752A1
; GENERAL INFORMATION:
; APPLICANT: Teruo Nishida
; APPLICANT: Masatsugu Nakamura
; TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
; FILE REFERENCE: 04355/HG
; CURRENT APPLICATION NUMBER: US/10/497,628
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: JP 2001-368103
; PRIOR FILING DATE: 2001-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-10-497-628-15

Query Match      80.0%; Score 20; DB 17; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5
Db 1 FFGLM 5

RESULT 12
US-10-168-789A-32
; Sequence 32, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Yasuaki
; APPLICANT: NISHI, Kazunori
; APPLICANT: KITADA, Chieko
; APPLICANT: INATOMI, No. US20030148943A1uhiro
; TITLE OF INVENTION: No. US20030148943A1el Tachykinin-like Polypeptides and Use Thereof
; FILE REFERENCE: 2680USOP
; CURRENT APPLICATION NUMBER: US/10/168,789A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: PCT/JP00/09083
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: JP 11-362638
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 12-066714
; PRIOR FILING DATE: 1999-03-10

; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 32
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Polypeptide
; NAME/KEY: PEPTIDE
; LOCATION: (02)..(02)
; OTHER INFORMATION: Xaa is any amino acid
US-10-168-789A-32

Query Match      68.0%; Score 17; DB 14; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5
Db 1 FXGLL 5

RESULT 13
US-10-497-628-16
; Sequence 16, Application US/10497628
; Publication No. US2005009752A1
; GENERAL INFORMATION:
; APPLICANT: Teruo Nishida
; APPLICANT: Makoto Inui
; APPLICANT: Masatsugu Nakamura
; TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
; FILE REFERENCE: 04355/HG
; CURRENT APPLICATION NUMBER: US/10/497,628
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: JP 2001-368103
; PRIOR FILING DATE: 2001-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-10-497-628-16

Query Match      68.0%; Score 17; DB 17; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5
Db 1 YFGLM 5

RESULT 14
US-08-484-409-30
; Sequence 30, Application US/08484409
; Publication No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-484-409-30

Query Match          64.0%; Score 16; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVG 3
Db 2 FVG 4

RESULT 15
US-10-033-026-2
; Sequence 2, Application US/10033026
; Publication No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Lipescombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-033-026-2

Query Match          64.0%; Score 16; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVG 3
Db 2 FVG 4

Search completed: March 23, 2005, 15:07:06
Job time : 93 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 14:37:21 ; Search time 30 Seconds  
(without alignments)  
12.442 Million cell updates/sec

Title: SEQ2

Perfect score: 25

Sequence: 1 fvglm 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 27945

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	80.0	5	1 US-07-753-909B-3	Sequence 3, Appli
2	20	80.0	5	1 US-07-934-553-2	Sequence 2, Appli
3	20	80.0	5	1 US-08-269-288-1	Sequence 1, Appli
4	20	80.0	5	1 US-08-225-474-2	Sequence 2, Appli
5	20	80.0	5	1 US-08-391-910-1	Sequence 1, Appli
6	20	80.0	5	1 US-08-418-994-1	Sequence 1, Appli
7	20	80.0	5	1 US-08-391-814-1	Sequence 1, Appli
8	20	80.0	5	1 US-08-441-591-61	Sequence 61, Appli
9	20	80.0	5	1 US-08-303-362A-61	Sequence 61, Appli
10	20	80.0	5	1 US-08-462-415-1	Sequence 1, Appli
11	20	80.0	5	1 US-08-463-874-1	Sequence 1, Appli
12	20	80.0	5	1 US-08-444-135-1	Sequence 1, Appli
13	20	80.0	5	1 US-08-318-391-1	Sequence 1, Appli
14	20	80.0	5	1 US-07-737-371B-6	Sequence 6, Appli
15	20	80.0	5	3 US-08-257-966-1	Sequence 1, Appli
16	20	80.0	5	3 US-09-265-690C-1	Sequence 1, Appli
17	20	80.0	5	3 US-09-265-690C-4	Sequence 4, Appli
18	20	80.0	5	4 US-08-153-847-1	Sequence 1, Appli
19	20	80.0	5	4 US-09-635-266-4	Sequence 4, Appli
20	20	80.0	5	4 US-10-230-133-4	Sequence 4, Appli
21	20	80.0	5	5 PCT-US95-05600-78	Sequence 78, Appli
22	19	76.0	5	1 US-07-690-284A-6	Sequence 6, Appli
23	17	68.0	5	2 US-07-737-371B-48	Sequence 48, Appli
24	16	64.0	4	1 US-08-127-904-2	Sequence 2, Appli
25	16	64.0	4	1 US-08-127-904-12	Sequence 12, Appli
26	16	64.0	4	3 US-08-638-407-24	Sequence 24, Appli
27	16	64.0	4	3 US-09-264-709A-11	Sequence 11, Appli

28	16	64.0	4	3 US-09-264-709A-33	Sequence 33, Appli
29	16	64.0	4	3 US-09-264-709A-35	Sequence 35, Appli
30	16	64.0	4	3 US-09-268-163-2	Sequence 2, Appli
31	16	64.0	4	5 PCT-US94-10475-2	Sequence 2, Appli
32	16	64.0	4	5 PCT-US94-10475-12	Sequence 12, Appli
33	16	64.0	5	1 US-07-690-284A-2	Sequence 2, Appli
34	16	64.0	5	1 US-08-127-904-1	Sequence 1, Appli
35	16	64.0	5	3 US-09-264-709A-27	Sequence 27, Appli
36	16	64.0	5	4 US-09-608-892-16	Sequence 16, Appli
37	16	64.0	5	5 PCT-US94-10475-1	Sequence 1, Appli
38	15	60.0	3	4 US-09-635-266-2	Sequence 2, Appli
39	15	60.0	3	4 US-10-230-133-2	Sequence 2, Appli
40	15	60.0	4	1 US-08-127-904-8	Sequence 8, Appli
41	15	60.0	4	1 US-08-441-591-63	Sequence 63, Appli
42	15	60.0	4	1 US-08-303-362A-63	Sequence 63, Appli
43	15	60.0	4	2 US-08-070-301-8	Sequence 8, Appli
44	15	60.0	4	3 US-09-265-690C-2	Sequence 2, Appli
45	15	60.0	4	4 US-09-635-266-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
US-07-753-909B-3  
; Sequence 3, Application US/07753909B  
; Patent No. 5304632  
; GENERAL INFORMATION:  
; APPLICANT: Vaudry, Hubert  
; APPLICANT: Conlon, Michael J.  
; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zarley, McKee, Thomte, Voorhees, and Sease  
; STREET: 801 Grand, Suite 3200  
; CITY: Des Moines  
; STATE: Iowa  
; COUNTRY: United States  
; ZIP: 50309  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07753,909B  
; FILING DATE: 19910903  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9106759  
; FILING DATE: 04-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sease, Edmund J.  
; REGISTRATION NUMBER: 24,741  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (515)-288-3667  
; TELEFAX: (515)-288-1338  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: C-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Rana ridibunda  
; DEVELOPMENTAL STAGE: adult  
; TISSUE TYPE: brain  
; US-07-753-909B-3

Query Match 80.0%; Score 20; DB 1; Length 5;  
Best Local similarity 80.0%; Pred. No. 4.1e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
Db 1 FXGLM 5

## RESULT 2

US-07-934-553-2  
; Sequence 2, Application US/07934553  
; Patent No. 5314690  
; GENERAL INFORMATION:  
; APPLICANT: PATTERSON, ROY  
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE  
; TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; STREET: 100 SOUTH WACKER DRIVE  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60606-4002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,553  
; FILING DATE: 19920821  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/705,071  
; FILING DATE: 24-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FENTRESS, SUSAN B  
; REGISTRATION/DOCKET NUMBER: NU-9033CIP  
; TELEPHONE: 312/456-8000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-07-934-553-2

Query Match 80.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
Db 1 FXGLM 5

## RESULT 3

US-08-269-288-1  
; Sequence 1, Application US/08269288  
; Patent No. 5491140  
; GENERAL INFORMATION:  
; APPLICANT: Bruns, Robert F.  
; APPLICANT: Gehlert, Donald R.  
; APPLICANT: Howbert, James J.  
; APPLICANT: Lunn, William H.W.  
; TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center/1104  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/269,288  
FILING DATE:

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9715  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-269-288-1

Query Match 80.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
Db 1 FXGLM 5

## RESULT 4

US-08-225-474-2  
; Sequence 2, Application US/08225474  
; Patent No. 5560915  
; GENERAL INFORMATION:  
; APPLICANT: Patterson, Roy  
; TITLE OF INVENTION: Method and Composition for Treating  
; TITLE OF INVENTION: IGE Mediated Allergies  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut  
; STREET: 100 S. Wacker Drive, Suite 960  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-4002  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,474  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,553  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/705,071  
; FILING DATE: 24-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tilton, Timothy L.

REGISTRATION NUMBER: 16,926  
REFERENCE/DOCKET NUMBER: NU 9033-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)-456-8000  
TELEFAX: (312)-456-7776  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-225-474-2

Query Match 80.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
DB 1 FFGLM 5

RESULT 5  
US-08-391-910-1  
Sequence 1, Application US/08391910  
Patent No. 5563133  
GENERAL INFORMATION:  
APPLICANT: Hipskind, Philip A.  
TITLE OF INVENTION: HEXAMETHYLENEMINYL TACHYKININ RECEPTOR  
TITLE OF INVENTION: ANTAGONISTS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/391,910  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9979  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-391-910-1

Query Match 80.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
DB 1 FFGLM 5

RESULT 6  
US-08-418-994-1  
Sequence 1, Application US/08418994  
Patent No. 5565568  
GENERAL INFORMATION:  
APPLICANT: Cho, Sung-Yong S.  
APPLICANT: Hipskind, Philip A.  
APPLICANT: Howbert, J. J.  
APPLICANT: Muehl, Brian S.  
APPLICANT: Nixon, James A.  
TITLE OF INVENTION: 2-ACYLAMINOPROPANAMIDES AS TACHYKININ  
TITLE OF INVENTION: RECEPTOR ANTAGONISTS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/418,994  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-8252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-418-994-1

Query Match 80.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
DB 1 FFGLM 5

RESULT 7  
US-08-391-814-1  
Sequence 1, Application US/08391814  
Patent No. 5607947  
GENERAL INFORMATION:  
APPLICANT: Hipskind, Philip A.  
TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR  
TITLE OF INVENTION: ANTAGONISTS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/391.814  
 FILING DATE:  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gaylo, Paul J.  
 REGISTRATION NUMBER: 36,808  
 REFERENCE/DOCKET NUMBER: X-9965  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317) 276-0756  
 TELEFAX: (317) 276-3861  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-391-814-1

Query Match 80.0%; Score 20; DB 1; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 | | | |  
 Db 1 FXGLM 5

## RESULT 8

US-08-441-591-61  
 Sequence 61, Application US/08441591  
 Patent No. 5637682  
 GENERAL INFORMATION:  
 APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
 TITLE OF INVENTION: HIGH-AFFINITY  
 TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
 TITLE OF INVENTION: TO THE TACHYKININ  
 TITLE OF INVENTION: SUBSTANCE P  
 NUMBER OF SEQUENCES: 66  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Swanson & Bratschun, L.L.C.  
 STREET: 8400 E. Prentice Avenue, Suite 200  
 CITY: Englewood  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/441,591  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/303,362  
 FILING DATE: 9-SEPTEMBER-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/714,131  
 FILING DATE: 10-JUNE-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/931,473  
 FILING DATE: 17-AUGUST-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/117,991  
 FILING DATE: 8-SEPTEMBER 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/536,428  
 FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/964,624  
 FILING DATE: 21-OCTOBER-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry J. Swanson  
 REGISTRATION NUMBER: 33,215  
 REFERENCE/DOCKET NUMBER: NEX21/C  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 793-3333  
 TELEFAX: (303) 793-3433  
 INFORMATION FOR SEQ ID NO: 61:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: Xaa  
 LOCATION: 2  
 OTHER INFORMATION: AROMATIC OR ALIPHATIC  
 OTHER INFORMATION: AMINO ACID  
 US-08-441-591-61

Query Match 80.0%; Score 20; DB 1; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
 | | | |  
 Db 1 FXGLM 5

## RESULT 9

US-08-303-362A-61  
 Sequence 61, Application US/08303362A  
 Patent No. 5648214  
 GENERAL INFORMATION:  
 APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
 TITLE OF INVENTION: HIGH-AFFINITY  
 TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
 TITLE OF INVENTION: TO THE TACHYKININ  
 TITLE OF INVENTION: SUBSTANCE P  
 NUMBER OF SEQUENCES: 66  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Swanson & Bratschun, L.L.C.  
 STREET: 8400 E. Prentice Avenue, Suite 200  
 CITY: Englewood  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/303,362A  
 FILING DATE: 9-SEPTEMBER-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/714,131  
 FILING DATE: 10-JUNE-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/931,473  
 FILING DATE: 17-AUGUST-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/117,991  
 FILING DATE: 8-SEPTEMBER 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/536,428  
 FILING DATE: 11-JUNE-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/964,624

```

; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: 2
; OTHER INFORMATION: AROMATIC OR ALIPHATIC
; OTHER INFORMATION: AMINO ACID
US-08-303-362A-61

```

```

Query Match      80.0%; Score 20; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 FVGLM 5
        |||
DB      1 FXGLM 5

```

```

RESULT 10
US-08-462-415-1
; Sequence 1, Application US/08462415
; Patent No. 5670499
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Crowell, Thomas A.
; APPLICANT: Gitter, Bruce D.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, Jeffry J.
; APPLICANT: Krushinski, Joseph H.
; APPLICANT: Lobb, Karen L.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: HETEROCYCLIC TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,415
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X8849B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3861
; TELEFAX: 317-276-0756
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids

```

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-462-415-1

```

```

Query Match      80.0%; Score 20; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 FVGLM 5
        |||
DB      1 FXGLM 5

```

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RESULT 11
US-08-463-874-1
; Sequence 1, Application US/08463874
; Patent No. 5684033
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung Y.
; APPLICANT: Crowell, Thomas A.
; APPLICANT: Gitter, Bruce D.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, Jeffry J.
; APPLICANT: Krushinski, Joseph H.
; APPLICANT: Lobb, Karen L.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: NON-PEPTIDE TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,874
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X8849C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-0756
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-874-1

```

```

Query Match      80.0%; Score 20; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 FVGLM 5
        |||
DB      1 FXGLM 5

```

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RESULT 12
US-08-444-135-1
; Sequence 1, Application US/08444135
; Patent No. 5723575
; GENERAL INFORMATION:
; APPLICANT: Gilon, Chaim
; APPLICANT: Zelinger, Zvi
; APPLICANT: Byk, Gerardo
; TITLE OF INVENTION: Backbone Cyclic Peptides, Processes For
; TITLE OF INVENTION: Their Preparation and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,135
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/955,380
; FILING DATE: 01-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarkovsky, Issac
; REGISTRATION NUMBER: 22,713
; REFERENCE/DOCKET NUMBER: 7754-003-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /label=Xaa
; OTHER INFORMATION: /note="Xaa = Phe or Val"
US-08-444-135-1
Query Match 80.0%; Score 20; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5
Db 1 FXGLM 5

RESULT 13
US-08-318-391-1
; Sequence 1, Application US/08318391
; Patent No. 574482
; GENERAL INFORMATION:
; APPLICANT: Cohen, Marlene L.
; APPLICANT: Johnson, Kirk W.
; APPLICANT: Prebus, Lee A.
; TITLE OF INVENTION: USE OF A SEROTONIN AGONIST IN
; TITLE OF INVENTION: COMBINATION WITH A TACHYKININ RECEPTOR ANTAGONIST IN THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF MIGRAINE

```

```

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,391
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9664
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-391-1
Query Match 80.0%; Score 20; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVGLM 5
Db 1 FXGLM 5

RESULT 14
US-07-737-371E-6
; Sequence 6, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066

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REFERENCE/DOCKET NUMBER: 00108/028002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-737-371B-6

Query Match 80.0%; Score 20; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
DB 1 FVGLM 5

RESULT 15  
US-08-257-966-1  
Sequence 1, Application US/08257966  
Patent No. 6175013  
GENERAL INFORMATION:  
APPLICANT: Hipskind, Philip A.  
APPLICANT: Howbert, James J.  
APPLICANT: Muehl, Brian S.  
TITLE OF INVENTION: IMIDAZOLINYL TACHYKININ RECEPTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center/1104  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/257,966  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9197  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-257-966-1

Query Match 80.0%; Score 20; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVGLM 5  
DB 1 FXGLM 5

Search completed: March 23, 2005, 14:50:59  
Job time : 31 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 15:03:13 ; Search time 38 seconds  
(without alignments)  
10.128 Million cell updates/sec

Title: SEQ3

Perfect score: 21

Sequence: 1 fglm 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.\*

2: PIR1.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	47.6	4	2 PT0240	Ig heavy chain CRD
2	10	47.6	4	2 A53284	T-cell receptor be
3	8	38.1	4	2 PT0633	T-cell receptor be
4	7	33.3	3	3 B23751	spinal cord peptid
5	7	33.3	4	2 B4823	synaptosomal-assoc
6	7	33.3	4	2 B3284	T-cell receptor be
7	6	28.6	3	3 PT0636	T-cell receptor be
8	6	28.6	3	3 PT0571	T-cell receptor be
9	6	28.6	3	3 S68328	blood cell protein
10	6	28.6	3	3 GXHU	growth-modulating
11	6	28.6	3	3 A50898	bursin - chicken
12	6	28.6	3	3 A23751	spinal cord peptid
13	6	28.6	4	1 ECKAA	antho-RFamide neur
14	6	28.6	4	2 D41654	hypothetical prote
15	6	28.6	4	2 S3508	starvation-induced
16	6	28.6	4	2 T30569	hypothetical prote
17	6	28.6	4	2 I38888	COI intron 16 prot
18	6	28.6	4	2 A25844	antho-RF amide neu
19	6	28.6	4	2 A34626	RPCH-related neuro
20	6	28.6	4	2 S39390	myosin-light-chain
21	6	28.6	4	2 S43959	Ig mu chain V regi
22	6	28.6	4	2 S47552	ubiquitin - rat
23	6	28.6	4	2 S09478	globulin IV alpha
24	6	28.6	4	2 PL0140	carbon-monoxide de
25	6	28.6	4	2 J01273	neuropeptide Antho
26	6	28.6	4	2 A35779	neuropeptide Antho
27	6	28.6	4	2 A60418	FMRFamide - polych
28	6	28.6	4	2 A32480	achatin-I - giant
29	6	28.6	4	2 PT0271	Ig heavy chain CRD

30 6 28.6 4 2 PT0711 T-cell receptor be  
31 6 28.6 4 2 PT0698 T-cell receptor be  
32 6 28.6 4 2 PT0677 T-cell receptor be  
33 6 28.6 4 2 PT0706 T-cell receptor be  
34 6 28.6 4 2 PT0675 T-cell receptor be  
35 6 28.6 4 2 PT0721 T-cell receptor be  
36 6 28.6 4 2 PT0566 T-cell receptor be  
37 6 28.6 4 2 A32039 tyrosine-melanocyt  
38 6 28.6 4 2 EGNK angiotensin-conver  
39 5 23.8 3 3 PQ0010 angiotensin-conver  
40 5 23.8 3 3 S13894 histidinol dehydro  
41 5 23.8 3 3 I50412 gene p20K protein  
42 5 23.8 3 3 PT0578 T-cell receptor be  
43 5 23.8 3 3 I78890 tyrosine protein k  
44 5 23.8 3 3 T13892 cytochrome-c oxida  
45 5 23.8 4 2 S18401 thyroglobulin - do

#### ALIGNMENTS

##### RESULT 1

PT0240

Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0240

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0240

A;Molecule type: DNA

A;Residues: 1-4 <YAM>

A;Experimental source: B lymphocyte

A;Keywords: heterotetramer; immunoglobulin

Query Match 47.6%; Score 10; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GL 3

Db 3 GL 4

##### RESULT 2

A53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C;Accession: A53284

R;Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A;Title: Evolutionarily conserved organization and sequences of germline diversity and j

A;Reference number: A53284; MUID:91342695; PMID:1678859

A;Accession: A53284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-4 <HAR>

A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19517.1; PID:g233917

A;Note: Sequence extracted from NCBI backbone (NCBIN:60737, NCBIIP:60739)

C;Keywords: T-cell receptor

Query Match 47.6%; Score 10; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GL 3

Db 1 GL 2

```

RESULT 3
PT0633
T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: PT0633
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0633
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEE>
A:Cross-references: UNIPROT:O8BIV7
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      38.1%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GL 3
      :|
Db      3 GI 4

RESULT 4
B23751
spinal cord peptide SCP-5 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C:Accession: B23751
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425; PMID:4015098
A:Accession: B23751
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <HSI>

Query Match      33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LM 4
      :|
Db      1 NM 2

RESULT 5
E44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N:Alternate names: superprotein peptide 1
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C:Accession: E44823
R:Loewy, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A:Reference number: A44823; MUID:92044785; PMID:1941090
A:Accession: E44823
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <LOE>
A:Experimental source: visual tissue
A:Note: sequence extracted from NCBI backbone (NCBIP:64247)
C:Keywords: membrane trafficking

Query Match      33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 LM 4
      :|
Db      1 IM 2

RESULT 6
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity and
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: B53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:S60737; NID:9233916; PIDN:AAB19518.1; PID:9233918
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C:Keywords: T-cell receptor

Query Match      33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 PG 2
      :|
Db      2 WG 3

RESULT 7
PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PT0636
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0636
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-3 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      28.6%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 G 2
      :|
Db      3 G 3

RESULT 8
PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PT0571
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0571
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-3 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c

```

## C;Keywords: T-cell receptor

Query Match 28.6%; Score 6; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 DB 3 G 3

## RESULT 9

S68328  
 blood cell protein A - Molgula manhattensis (fragment)  
 C;Species: Molgula manhattensis  
 C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C;Accession: S68328  
 R;Taylor, S.W.; Ross, M.M.; Waite, J.H.  
 Arch. Biochem. Biophys. 324, 228-240, 1995  
 A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from the blood cell protein A of *Molgula manhattensis*  
 A;Reference number: S68328; PMID:8554314  
 A;Accession: S68328  
 A;Molecule type: protein  
 A;Residues: 1-3 <TRY>

Query Match 28.6%; Score 6; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 DB 2 F 2

## RESULT 10

GKHU  
 growth-modulating peptide - human  
 C;Species: Homo sapiens (man)  
 C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
 C;Accession: A01421  
 R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.  
 Experientia 33, 324-325, 1977  
 A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.  
 A;Reference number: A01421; PMID:77162369; PMID:858356  
 A;Accession: A01421  
 A;Molecule type: protein  
 A;Residues: 1-3 <SCH>  
 A;Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit growth-modulating peptide - human

Query Match 28.6%; Score 6; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 DB 1 G 1

## RESULT 11

A60898  
 bursin - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
 C;Accession: A60898  
 R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.  
 Science 231, 997-999, 1986  
 A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the bursa of Fabricius  
 A;Reference number: A60898; PMID:86122916; PMID:3484838  
 A;Accession: A60898  
 A;Molecule type: protein  
 A;Residues: 1-3 <AUD>  
 A;Keywords: amidated carboxyl end; hormone  
 C;3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 6; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 DB 3 G 3

## RESULT 12

A23751  
 spinal cord peptide SCP-4 - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
 C;Accession: A23751  
 R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, F.  
 Arch. Biochem. Biophys. 240, 178-183, 1985  
 A;Reference number: A23751; PMID:85250425; PMID:4015098  
 A;Accession: A23751  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-3 <HSI>

Query Match 28.6%; Score 6; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 DB 2 G 2

## RESULT 13

ECXAA  
 antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)  
 C;Species: Anthopleura elegantissima  
 C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
 C;Accession: A26666  
 R;Grimmelikhuijzen, C.J.P.; Graff, D.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986  
 A;Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anemone  
 A;Reference number: A26666; PMID:87092339; PMID:2879288  
 A;Accession: A26666  
 A;Molecule type: protein  
 A;Residues: 1-4 <GRI>

A;Cross-references: UNIPROT:P10419  
 A;Comment: The function of this peptide is not known but it could act as a transmitter and modulate the function of natural peptides had identical properties.  
 C;Superfamily: RFamide neuropeptide  
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 DB 2 G 2

## RESULT 14

D41654  
 hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)  
 C;Species: Haemophilus parainfluenzae  
 C;Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 24-Feb-1995  
 C;Accession: D41654  
 R;Kroll, J.S.; Langford, P.R.; Loynds, B.M.  
 J. Bacteriol. 173, 7449-7457, 1991  
 A;Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus para  
 A;Reference number: A41654; PMID:92041655; PMID:1938942

A;Accession: D41654  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-4 <KRO>

Query Match 28.6%; Score 6; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
|  
Db 3 F 3

## RESULT 15

S53508  
starvation-induced ribonuclease - tomato  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
C;Accession: S53508  
R;Koeck, M.; Loeffler, A.; Abel, S.; Giund, K.  
Plant Mol. Biol. 27, 477-485, 1995  
A;Title: cDNA structure and regulatory properties of a family of starvation-induced ribonucleases  
A;Reference number: S53506; MUID:95201242; PMID:7894013  
A;Accession: S53508  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-4 <KOE>

Query Match 28.6%; Score 6; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
|  
Db 1 F 1

Search completed: March 23, 2005, 15:13:39  
Job time : 38 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:51:07 ; Search time 171 Seconds  
(without alignments)  
11.978 Million cell updates/sec

Title: SEQ3  
Perfect score: 21  
Sequence: 1 fg1m 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	57.1	4	1 OCP1_OCTMI	P58648 octopus min
2	9	42.9	4	1 ILME SEPOF	P83568 sepia offic
3	6	28.6	2	1 GWA SEPOF	P83570 sepia offic
4	6	28.6	3	1 GRM1_HUMAN	P01157 homo sapien
5	6	28.6	4	1 ACH1_ACHFU	P35904 achatina fu
6	6	28.6	4	1 DGLM_PSECH	P19916 pseudomonas
7	6	28.6	4	1 E0S1_HUMAN	P02731 homo sapien
8	6	28.6	4	1 FAR3_HIRME	P42562 hirudo medi
9	6	28.6	4	1 FAR4_HIRME	P42563 hirudo medi
10	6	28.6	4	1 FPKA_ATEL	P58705 anthopleura
11	6	28.6	4	1 FLRP_HIRME	P42561 hirudo medi
12	6	28.6	4	1 FLRN_ATEL	P58707 anthopleura
13	6	28.6	4	1 FMRP_MACNI	P01162 macrocallis
14	6	28.6	4	1 FYRI_ATEL	P58706 anthopleura
15	6	28.6	4	1 OCP3_OCTMI	P58649 octopus min
16	6	28.6	4	2 Q16047	Q16047 homo sapien
17	5	23.8	4	1 DCNS_PSECH	P19918 pseudomonas
18	5	23.8	4	2 Q9GAT0	Q9GAT0 homo sapien
19	4	19.0	4	2 Q08433	Q08433 rattus sp.
20	2	9.5	3	1 LUXE_VIBFI	P24272 vibrio fisc
21	1	4.8	4	1 YLM1_YEAST	P36515 saccharomyc
22	0	0.0	3	1 THYL_BOMOR	P62970 bombina ori
23	0	0.0	3	1 THYL_NOTVI	P63971 notophthalm
24	0	0.0	3	1 THYL_PIG	P62968 sus scrofa
25	0	0.0	3	1 THYL_SHEEP	P62969 ovis aries
26	0	0.0	4	1 TUPT_HUMAN	P01858 homo sapien

## ALIGNMENTS

```

RESULT 1
OCP1_OCTMI
ID OCP1_OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hiaada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less active
CC than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI; RANGE=1-4; NOTE=Ref.1.
KW D-amino acid; Direct protein sequencing; Hormone.
FT MOD RES 2 2 D-phenylalanine (in form Ocp-1).
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 57.1%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FG 2
Db 2 FG 3

RESULT 2
ILME SEPOF
ID ILME SEPOF STANDARD; PRT; 4 AA.
AC P83568;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pheromone peptide ILME.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Egg;
RX MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;
RA Zatylny C., Gagnon J., Boucaud-Camou S., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis.";
RL Biochem. Biophys. Res. Commun. 275:217-222(2000).
RN [2]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=2197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -!- FUNCTION: Has myotropic activity targeting the genital tract.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg (EC2).
CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=WALDI; RANGE=1-4; NOTE=Ref.1.
KW Direct protein sequencing; Pheromone.

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SQ SEQUENCE 4 AA; 505 MW; 6B169720300000000 CRC64;

Query Match 42.9%; Score 9; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LM 4  
 . | |  
 Db 2 LM 3

RESULT 3  
 GWA\_SEPOF  
 ID GWA\_SEPOF STANDARD; PRT; 2 AA.  
 AC P83570; 2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide GWA.  
 OS Sepia officinalis (Common cuttlefish).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
 OX NCBI\_TaxID=6610;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Optic lobe;  
 RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;  
 RA Henry J., Favrel P., Boucaud-Camou E.;  
 RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
 peptide inhibiting the motility of the mature oviduct in the  
 cuttlefish, *Sepia officinalis*.";  
 RL Peptides 18:1469-1474 (1997).  
 CC -1- FUNCTION: Regulatory neuropeptide with myotropic activity  
 targeting the distal oviduct. Inhibits the motility of the oviduct  
 by decreasing tone, frequency and amplitude of contractions.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD RES 2 2 Tryptophan amide.  
 SQ SEQUENCE 2 AA; 261 MW; 7378100000000000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 . |  
 Db 1 G 1

RESULT 4  
 GRWM\_HUMAN  
 ID GRWM\_HUMAN STANDARD; PRT; 3 AA.  
 AC P01157;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Growth-modulating peptide.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77162369; PubMed=858356;  
 RA Schlesinger D.H., Pickart L., Thaler M.M.;  
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
 RL Experientia 33:324-325 (1977).  
 CC -1- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
 growth of some cell types and to inhibit other types in vitro.  
 CC GO: GO:0001558; P:regulation of cell growth; NAS.  
 DR Direct protein sequencing.  
 KW SEQUENCE 3 AA; 340 MW; 6331E81000000000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 . |  
 Db 1 G 1

RESULT 5  
 ACHI\_ACHFU  
 ID ACHI\_ACHFU STANDARD; PRT; 4 AA.  
 AC P35904;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Achatina-I.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN=Perussac; TISSUE=Ganglion;  
 RX MEDLINE=89273551; PubMed=2597281;  
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 fulica Ferussac containing a D-amino acid residue.";  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020 (1989).  
 CC [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=Perussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;  
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 Achatina fulica, and its possible function.";  
 RL Biochem. Biophys. Res. Commun. 177:847-853 (1991).  
 CC [3]  
 RP CRYSTALLIZATION.  
 RX MEDLINE=93014523; PubMed=1392265;  
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
 Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid  
 residue.";  
 RL Int. J. Pept. Protein Res. 39:258-264 (1992).  
 CC -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
 and produces a spike broadening of the identified heart excitatory  
 neuron (PON); also enhances the amplitude and frequency of the  
 heart beat. Has also an effect on several other muscles.

DR PIR; A32480; A32480.  
 KW D-amino acid; Direct 2 D-phenylalanine.  
 FT MOD RES 2  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C8100000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 G 2  
 . |  
 Db 1 G 1

RESULT 6  
 DCML\_PSSCH  
 ID DCML\_PSSCH STANDARD; PRT; 4 AA.  
 AC P19916;  
 DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).  
 GN Name=cutL;  
 OS Pseudomonas carboxydohydrogena.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae.  
 OX NCBI\_TaxID=290;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of CO dehydrogenase structural genes in  
 RT carboxydotrophic bacteria.";  
 RL Arch. Microbiol. 152:335-341(1989).  
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
 CC dioxide.  
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
 CC -1- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum (VI) ion and 1  
 CC molybdopterin cytosine dinucleotide (MCD) per subunit.  
 CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
 CC subunit.  
 DR PIR; PLO140; PLO140.  
 KW Direct protein sequencing; Molybdenum; Oxidoreductase.  
 FT NON\_TER 4 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761B876F0000000 CRC64;  
  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;  
 Matches 1; Conservative 0; Mismatches 0;  
  
 QY 2 G 2  
 Db |  
 2 G 2  
  
 RESULT 7  
 EOSI\_HUMAN STANDARD; PRT; 4 AA.  
 ID EOSI\_HUMAN  
 AC P02731;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Eosinophilic tetrapeptides.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76078412; PubMed=1060093;  
 RA Goetzl E.J., Austen K.F.;  
 RT "Purification and synthesis of eosinophilic tetrapeptides of  
 RT human lung tissue: identification as eosinophil chemotactic factor of  
 RT anaphylaxis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -1- MISCELLANEOUS: These peptides are released from mast cells in lung  
 CC (and other tissues) during hypersensitivity reactions  
 CC (anaphylaxis). Their activities, preferentially affecting  
 CC eosinophils, include chemotaxis, chemotactic deactivation, release  
 CC of enzymes, and stimulation of the hexose monophosphate shunt.  
 DR GO; GO:0006935; P:chemotaxis; IDA.  
 DR GO; GO:0006955; P:immune response; IDA.  
 KW Direct protein sequencing.  
 FT VARIANT 1 1 V -> A (in other peptide).  
 FT 1 /FTID=VAR\_005201.  
 SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;  
  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;  
 Matches 1; Conservative 0; Mismatches 0;

QY 2 G 2  
 Db |  
 2 G 2  
  
 RESULT 8  
 FAR3\_HIRME STANDARD; PRT; 4 AA.  
 ID FAR3\_HIRME  
 AC P42562;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRFamide-like neuropeptide YLRF-amide.  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamde neuropeptides in the medicinal leech.";  
 RL Peptides 12:897-908(1991).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 4 4 Phenylalanine amide.  
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;  
  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;  
 Matches 1; Conservative 0; Mismatches 0;  
  
 QY 1 F 1  
 Db |  
 4 F 4  
  
 RESULT 9  
 FAR4\_HIRME STANDARD; PRT; 4 AA.  
 ID FAR4\_HIRME  
 AC P42563;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRFamide-like neuropeptide YMRP-amide.  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamde neuropeptides in the medicinal leech.";  
 RL Peptides 12:897-908(1991).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 4 4 Phenylalanine amide.  
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;  
  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Indels 0; Gaps 0;  
 Matches 1; Conservative 0; Mismatches 0;  
  
 QY 1 F 1  
 Db |  
 4 F 4

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RESULT 10
FFKA ANTEL          STANDARD;      PRT;      4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-KAamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide); a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
DR PIR; JQ1273; JQ1273.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Alanine amide.
SQ SEQUENCE 4 AA; 512 MW; 5D339C9A00000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 11
FLRF_HIRME          STANDARD;      PRT;      4 AA.
AC F42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FLRFamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhychochellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RX SPECIES-H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RX SPECIES-H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."

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RL Peptides 15:31-36(1994).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 582 MW; 69D40729A000000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 12
FLRN ANTEL          STANDARD;      PRT;      4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Rinscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT anemone neuropeptide containing an unusual amino-terminal blocking
RT group."
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FA; RANGE=1-4; NOTE=Ref.1.
DR PIR; A35779; A35779.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Asparagine amide.
SQ SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;

Query Match 28.6%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 13
FMRF_MACNI          STANDARD;      PRT;      4 AA.
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocaltista nimosa (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Helisoma trivolvis (Medicinal leech), and
OS Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC Veneroidae; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
RN [1]
RP SEQUENCE, AND SYNTHESIS.

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RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;  
 RX MEDLINE=77215956; PubMed=877592;  
 RA Price D.A., Greenberg M.J.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide.";  
 RL Science 197;670:117(1977).  
 RN [2]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;  
 RX MEDLINE=78012038; PubMed=909875;  
 RA Price D.A., Greenberg M.J.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide  
 from the central ganglia of a bivalve mollusc.";  
 RL Prep. Biochem. 7:261-281(1977).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=N.virens;  
 RX MEDLINE=90259866; PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;  
 RA Krajncik K.G., Price D.A.;  
 RT "Authentic FMRFamide is present in the polychaete Nereis virens.";  
 RL Peptides 11:75-77(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=H.medicinalis;  
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamamide neuropeptides in the medicinal leech.";  
 RL Peptides 12:897-908(1991).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=H.trivoltis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 trivoltis.";  
 RL Peptides 15:31-36(1994).  
 CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
 activities include augmentation, induction, and regularization of  
 cardiac contraction.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 family.  
 DR PIR; A01426; ECKN.  
 DR PIR; A60418; A60418.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD RES 4 4 Phenylalanine amide.  
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 F 1  
 Db 1 F 1  
 RESULT 14  
 ID\_FYRI ANTEL STANDARD; PRT; 4 AA.  
 AC P58706;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Antho-Riamide I (Contains: Antho-Riamide II).  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaea; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z;  
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
 RA Grimmelikhuijzen C.J.P.;

RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
 biologically active L-3-phenylactyl-Tyr-Arg-Ile-NH2 and its des-  
 phenylactyl fragment Tyr-Arg-Ile-NH2.";  
 RL Peptides 12:1165-1173(1991).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=93391436; PubMed=8397415;  
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
 RT "The expansion behaviour of sea anemones may be coordinated by two  
 inhibitory neuropeptides, Antho-Riamide and Antho-Riamide.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).  
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
 groups. May be involved in the expansion phase of feeding  
 behaviour in sea anemones.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Neuron specific.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT CHAIN 1 4 Antho-Riamide I.  
 FT CHAIN 2 4 Antho-Riamide II.  
 FT MOD RES 1 1 3-phenylactic acid.  
 FT MOD\_RES 4 4 Isoleucine amide.  
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 F 1  
 Db 1 F 1  
 RESULT 15  
 ID\_OCP3 OCTMI STANDARD; PRT; 4 AA.  
 AC P58649;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 Octopus minor.";  
 RL Peptides 21:623-630(2000).  
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
 inotropic effects on the heart. Ocp-4 is a 1000 time less active  
 than Ocp-3.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD RES 2 2 D-serine (in form Ocp-4).  
 SQ SEQUENCE 4 AA; 463 MW; 6AB35B8100000000 CRC64;  
 Query Match 28.6%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 G 2  
 Db 1 G 1  
 Search completed: March 23, 2005, 15:10:03  
 Job time : 172 secs

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OM protein - protein search, using sw model

Run on: March 23, 2005, 14:52:02 ; Search time 164 Seconds  
(without alignments)  
9.433 Million cell updates/sec

Title: SEQ3

Perfect score: 21

Sequence: 1 fglm 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 19815

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	2 AAW41683	AAW41683 Peptide u
2	21	100.0	4	2 AAY31075	Aay31075 Non-cross
3	21	100.0	4	3 AAB23026	Aab23026 Human/rat
4	21	100.0	4	3 AAY67577	Aay67577 P antagonist
5	21	100.0	4	4 AAB91447	Aab91447 Tachykini
6	21	100.0	4	5 ABB10091	Abb10091 Substance
7	21	100.0	4	5 AAU77846	Aau77846 Tachykini
8	21	100.0	4	7 ADE94198	Ad94198 High acti
9	21	100.0	4	8 ADR43772	Adr43772 Human mag
10	18	85.7	4	1 AAP61654	Aap61654 Sequence
11	18	85.7	4	1 AAP71301	Aap71301 Peptide c
12	18	85.7	4	2 AAW41686	Aaw41686 Tetrapept
13	18	85.7	4	5 ABB10092	Abb10092 Substance
14	16	76.2	4	1 AAP61707	Aap61707 Sequence
15	16	76.2	4	1 AAP71312	Aap71312 Peptide c
16	16	76.2	4	2 AAY23485	Aay23485 V beta 6
17	16	76.2	4	3 AAB12293	Aab12293 Prodrug o
18	16	76.2	4	4 AAG62847	Aag62847 Typical t
19	16	76.2	4	5 ABB88046	Abb88046 Enzyme cl
20	16	76.2	4	8 ADL78809	Adl78809 Exemplary
21	15	71.4	3	3 AAY67578	Aay67578 P antagonist
22	15	71.4	3	4 AAB91448	Aab91448 Tachykini
23	15	71.4	4	1 AAP60334	Aap60334 Peptide w
24	15	71.4	4	2 AAW77469	Aaw77469 Tetrapept
25	15	71.4	4	2 AAW41684	Aaw41684 Tetrapept

26	15	71.4	4	2 AAW41685	Aaw41685 Tetrapept
27	15	71.4	4	4 AAB91795	Aab91795 Amyloid b
28	15	71.4	4	4 AAB91822	Aab91822 Amyloid b
29	14	66.7	4	1 AAP61659	Aap61659 Sequence
30	14	66.7	4	1 AAP71306	Aap71306 Peptide c
31	14	66.7	4	2 AAR34486	Aar34486 FGIA. 8/1
32	14	66.7	4	2 AAR46020	Aar46020 Serine pr
33	14	66.7	4	2 AAR93149	Aar93149 Mycobacte
34	14	66.7	4	3 AAB12292	Aab12292 Prodrug o
35	14	66.7	4	4 AAB91714	Aab91714 Opioid pe
36	14	66.7	4	5 ABB88045	Abb88045 Enzyme cl
37	14	66.7	4	5 ABG32223	Abg32223 Sheep col
38	14	66.7	4	8 ADQ91509	Adq91509 HIV trunc
39	14	66.7	4	8 ADS77483	Ads77483 Ovine col
40	13	61.9	3	5 ABG77484	Abg77484 Targettin
41	13	61.9	4	1 AAP61658	Aap61658 Sequence
42	13	61.9	4	1 AAP71287	Aap71287 Opiate bi
43	13	61.9	4	1 AAP82691	Aap82691 Renin inh
44	13	61.9	4	2 AAR15768	Aar15768 Parnesyl-
45	13	61.9	4	2 AAR47299	Aar47299 Peptide a

## ALIGNMENTS

### RESULT 1

AAW41683

ID AAW41683 standard; peptide; 4 AA.

XX AC AAW41683;

XX DT 09-JUN-1998 (first entry)

XX DE Peptide used in ophthalmic drug to treat corneal disorders.

XX KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;

XX KW keratitis; insulin like growth factor-I; IGF-I; eye drop.

XX OS Synthetic.

XX PH Key Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"

XX PN WO9749419-A1.

XX PD 31-DEC-1997.

XX PF 11-JUN-1997; 97WO-JP002015.

XX PR 26-JUN-1996; 96JP-00165612.

XX PA (SANT ) SANTEN PHARM CO LTD.

XX PI Nishida T, Nakamura M, Nakata K;

XX DR WPI; 1998-076907/07.

XX PT Ophthalmic drug composition containing tetra-peptide - is useful as

XX PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,

XX PS Claim 1; Page 15; 19pp; Japanese.

XX CC The present sequence represents a tetrapeptide which is the active

XX CC ingredient in an ophthalmic drug composition. It is used, together with

XX CC insulin like growth factor-I (IGF-I), to treat corneal disorders such as

XX CC corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The

XX CC dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and

XX CC 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of

XX CC the composition is eye drops

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
 Db 1 FGLM 4

RESULT 2  
 AAY31075  
 ID AAY31075 standard; peptide; 4 AA.  
 AC AAY31075;  
 XX  
 XX 21-OCT-1999 (first entry)  
 XX  
 XX Non-crosslinked protein particle peptide 124.  
 XX  
 XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
 KW albumin; haemoglobin; nanometer; micrometer; clearance.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 4 /note= "C-terminal amide"  
 FT  
 XX US5945033-A.  
 FN  
 XX 31-AUG-1999.  
 PD  
 XX 12-NOV-1996; 96US-00747137.  
 PF  
 XX 15-JAN-1991; 91US-00641720.  
 PR 13-OCT-1992; 92US-00959560.  
 PR 01-JUN-1993; 93US-00069831.  
 PR 14-MAR-1994; 94US-00212546.  
 XX  
 XX (HEMO-) HEMOSPHERE INC.  
 PA  
 XX Yen RCK;  
 PI  
 XX WPI; 1999-508153/42.  
 DR  
 XX Non-crosslinked protein particles for therapeutic and diagnostic use.  
 FT  
 XX Example 22; Col 103-104; 65pp; English.  
 PS  
 XX This invention describes a novel aqueous suspension of monodisperse  
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is  
 CC stable against dissolving upon dilution with an alcohol-free aqueous  
 CC medium. The method involves (a) forming an aqueous solution containing  
 CC albumin and hemoglobin and (b) treating the aqueous solution with an  
 CC alcohol to cause the solution to become turbid. The particles are useful  
 CC as agents for in vivo administration, either of their own administration  
 CC or as a vehicle for other therapeutic or diagnostic agents. The method  
 CC permits the formation of albumin and hemoglobin particles in the  
 CC nanometer and micrometer size range, in a form closer to their natural  
 CC form than the forms of the prior art. The particles therefore constitute  
 CC a more closely controlled agent for in vivo administration, with greater  
 CC ease of clearance from the body after their period of usefulness.  
 CC AAY30952-Y31135 represent peptides used in the method of the invention  
 XX  
 XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
 Db 1 FGLM 4

RESULT 4  
 AAY67577  
 ID AAY67577 standard; peptide; 4 AA.  
 XX

Db 1 FGLM 4

RESULT 3  
 AAB23026  
 ID AAB23026 standard; peptide; 4 AA.  
 XX  
 AC AAB23026;  
 XX  
 XX 16-JAN-2001 (first entry)  
 DT  
 XX Human/rat tachykinin Substance P C-terminal tetrapeptide.  
 DE  
 XX Substance P; tachykinin; human; rat; magnesium binding defect;  
 KW sodium sensitive essential hypertension; insulin resistance;  
 KW type 2 diabetes; antibody; immunoassay; quantification.  
 XX  
 OS Homo sapiens.  
 OS Rattus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 4 /note= "C-terminal amide"  
 FT  
 XX WO200054053-A1.  
 FN  
 XX 14-SEP-2000.  
 PD  
 XX 09-MAR-2000; 2000WO-US003707.  
 PF  
 XX 10-MAR-1999; 99US-00265690.  
 PR  
 XX (WELL/) WELLS I C.  
 PA  
 XX Wells IC;  
 PI  
 XX WPI; 2000-587457/55.  
 DR  
 XX  
 XX Detecting magnesium binding defects associated with abnormal  
 PT physiological states such as sodium-sensitive essential hypertension and  
 PT type 2 insulin-resistant diabetes mellitus, comprises measuring a  
 PT specific pentapeptide in blood.  
 XX  
 PS Disclosure; Page 5; 21pp; English.  
 XX  
 CC The invention relates to a method for detecting magnesium binding  
 CC defects. The method comprises quantitating a tachykinin C-terminal  
 CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,  
 CC AAB23026) in blood using an antibody specific for the generalised  
 CC mammalian tachykinin C-terminal pentapeptide Phe-(Phe/Val)-Gly-Leu-Met-  
 CC NH2 (AAB23028). The method is useful for detecting cellular magnesium  
 CC binding defects which are associated with abnormal physiological states  
 CC such as sodium-sensitive essential hypertension and type 2 diabetes  
 CC mellitus. The present sequence represents the C-terminal 4 amino acids of  
 CC the tachykinin Substance P (AAB23027) from human and rat. This is a  
 CC degradation product of the Substance P C-terminal pentapeptide (AAB23025)  
 CC and may also be assayed according to the method of the invention  
 XX  
 XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
 Db 1 FGLM 4

RESULT 4  
 AAY67577  
 ID AAY67577 standard; peptide; 4 AA.  
 XX

AC AAY67577;  
 XX 19-MAY-2000 (first entry)  
 XX P antagonist peptide #5.  
 XX Pharmaceutical; veterinary; gonadotropin-releasing hormone; GnRH;  
 KW pore-forming agent; lecithin; stearin; P antagonist.  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 4  
 FT /note= "C-terminal amide"  
 FT  
 XX WO200004897-A1.  
 XX 03-FEB-2000.  
 XX 20-JUL-1999; 99WO-AU000585.  
 XX 20-JUL-1998; 98AU-00004730.  
 PR 20-JUL-1998; 98AU-00004731.  
 PR 13-MAY-1999; 99AU-00000324.  
 XX (PEPT-) PEPTTECH LTD.  
 PA Trigg TE, Walsh JD, Rathjen DA;  
 PI WPI; 2000-182528/16.  
 XX Bioimplant formulation for sustained delivery of an active agent over 7  
 PT days to 2 years, comprises active agent, pore-forming agent and stearin.  
 PT Claim 20; Page 21; 37pp; English.  
 XX The invention provides a pharmaceutical and/or veterinary formulation  
 CC that comprises 2 -30% of active agents which include a gonadotropin-  
 CC releasing hormone (GnRH) agonist, 0.5 - 20% of a pore-forming agent which  
 CC is not lecithin, and the remainder stearin. The formulation is useful as  
 CC a sustained release implant which can deliver the active agent for a  
 CC period of 7 days to 2 years. Sequences AAY67573-578 represent P  
 CC antagonist peptides used in the composition  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 3; Length 4;  
 Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLM 4  
 RESULT 5  
 AAB91447  
 ID AAB91447 standard; peptide; 4 AA.  
 XX AAB91447;  
 XX 22-JUN-2001 (first entry)  
 DT Tachykinins peptide SEQ ID NO:623.  
 DE Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200069900-A2.  
 PN

XX 23-NOV-2000.  
 PD 17-MAY-2000; 2000WO-US013576.  
 XX 17-MAY-1999; 99US-0134406P.  
 PR 10-SEP-1999; 99US-0153406P.  
 PR 15-OCT-1999; 99US-0159783P.  
 XX (CONJ-) CONJUCHEM INC.  
 PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 PI WPI; 2001-112059/12.  
 XX Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity.  
 PT Disclosure; Page 402; 733pp; English.  
 FS The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (II) and a  
 CC reactive group (III) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLM 4  
 RESULT 6  
 ABB10091  
 ID ABB10091 standard; peptide; 4 AA.  
 XX ABB10091;  
 AC 26-JUL-2002 (first entry)  
 XX Substance P analog used in wound healing treatment#14.  
 DT Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;  
 XX surgical incision; burn.  
 DE Unidentified.  
 XX WO200213853-A1.  
 XX 21-FEB-2002.  
 PD 10-AUG-2001; 2001WO-JP006933.  
 PF 10-AUG-2000; 2000JP-00242489.  
 XX 28-NOV-2000; 2000JP-00361388.  
 XX



CC promoting wound healing in the skin. The keratic injury is particularly  
 CC corneal ulcer, exfoliation of corneal epithelium, keratitis or dry eye.  
 CC The skin wound can be scratches, surgical cutting, skin ulcer, or burns.  
 CC This sequence represents one of the peptides of the invention with IGF-1  
 CC activity.  
 XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 21; DB 7; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 Db 1 FGLM 4

RESULT 9  
 ADR43772  
 ID ADR43772 standard; peptide; 4 AA.  
 AC ADR43772;  
 DT 18-NOV-2004 (first entry)  
 XX Human magnesium binding defect (MgBD) peptide mimetic #2.  
 DE  
 XX Magnesium binding defect; MgBD; MgBD binding defect peptide mimetic;  
 KW physiological disorder; preclampsia; pregnancy;  
 KW salt-sensitive essential hypertension; type 2 diabetes mellitus; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /label= OTHER  
 FT /note= "OTHER= C-terminal amide"  
 PN US2004171093-A1.  
 XX  
 PD 02-SEP-2004.  
 XX  
 PF 22-MAR-2004; 2004US-00805881.  
 XX  
 PR 10-MAR-1999; 99US-00265690.  
 PR 09-AUG-2000; 2000US-00635266.  
 PR 24-JAN-2002; 2002US-00053669.  
 PR 29-AUG-2002; 2002US-00230133.  
 PR 28-OCT-2003; 2003US-00695536.  
 XX  
 PA (WELL/) WELLS I C.  
 PI Wells IC;  
 XX  
 DR WPI; 2004-625105/60.  
 XX  
 PT Assessing predisposition to physiological disorder associated with  
 PT magnesium binding defect in individual by measuring level of amidated  
 PT peptides associated with magnesium binding defect in sample and comparing  
 PT peptide level to standard.  
 XX  
 PS Claim 1; SEQ ID NO 2; 21pp; English.  
 XX  
 CC The invention relates to a method of assessing a predisposition to a  
 CC physiological disorder associated with a magnesium binding defect in an  
 CC individual, involving measuring the level of amidated peptides associated  
 CC with the magnesium binding defect in a sample of body fluid of the  
 CC individual and comparing the level of peptide to a standard, where a  
 CC significantly lower level of the peptide is indicative of a  
 CC predisposition of the individual to the physiological disorder. The  
 CC invention also relates to a method of monitoring progress in treatment of  
 CC a physiological disorder associated with a magnesium binding defect in an  
 CC individual, involving comparing the level of peptide to the level of

CC peptide after treatment, where a significant increase in the level of the  
 CC peptide is indicative of the progress of treatment of the individual, a  
 CC monoclonal antibody that specifically binds to a peptide or its peptide  
 CC mimetic, a prognosis reagent for determining the presence of a magnesium  
 CC binding defect, generating a deficit of plasma membrane tightly bound  
 CC magnesium ion in mammalian somatic cells involving obtaining a sample of  
 CC body fluid comprising somatic cells, collecting the somatic cells from  
 CC the body fluid by centrifugation, resuspending the somatic cells in a  
 CC cell stabilising buffer, removing a sample of the suspended somatic  
 CC cells, measuring the level of tightly bound magnesium ion in the sample  
 CC of the somatic cells and repeating the removing and measuring steps at  
 CC subsequent times until the level of tightly bound magnesium is  
 CC significantly reduced and the somatic cells remain intact, a method of  
 CC identifying substances which promote binding of tightly bound magnesium  
 CC ion to a plasma membrane of mammalian somatic cells involving suspending  
 CC mammalian somatic cells having a deficit of plasma membrane tightly bound  
 CC magnesium in a physiological medium including magnesium ion, adding a  
 CC substance to be tested to the suspension and measuring the level of  
 CC tightly bound magnesium ion in the plasma membrane of the somatic cells  
 CC where a significant increase in the level of plasma membrane tightly  
 CC bound magnesium after addition of the substance to be tested is  
 CC indicative of promotion of binding by the substance, and a method for  
 CC ameliorating or correcting a magnesium binding defect in an individual  
 CC involving administering to the individual a substance which promotes  
 CC binding of tightly bound magnesium ion to the plasma membrane of  
 CC mammalian somatic cells. The methods are useful for assessing a  
 CC predisposition to a physiological disorder associated with a magnesium  
 CC binding defect in an individual, where the disorder is a predisposition  
 CC to preclampsia during pregnancy, salt-sensitive essential hypertension  
 CC or type 2 diabetes mellitus associated with the magnesium binding defect.  
 CC The method is also useful for ameliorating or correcting a magnesium  
 CC binding defect (MgBD) in an individual. This sequence represents a human  
 CC MgBD mimetic peptide of the invention.  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 8; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 ||||  
 Db 1 FGLM 4

RESULT 10

AAP61654

ID AAP61654 standard; peptide; 4 AA.

XX

AC AAP61654;

XX

DT 25-MAR-2003 (revised)

DT 03-OCT-2002 (revised)

DT 21-AUG-1991 (first entry)

XX

DE Sequence of peptide which inhibits cyclic-nucleotide independent protein  
 DE kinase activity and mammalian cell growth.

XX

KW Cell growth inhibitor; tumour cell growth inhibitor.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Misc-difference 1

FT /label= Carbobenzoxo-Phe

FT Misc-difference 4

FT /label= Leu-CH2Cl

XX

PN US4582821-A.

XX

PD 15-APR-1986.

XX

PP 16-NOV-1983; 83US-00552255.

XX PR 16-NOV-1983; 83US-00552255.  
 XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX PI Kettner CA, Racker E;  
 XX DR WPI; 1986-118872/18.  
 XX PT Inhibition of tumour cell growth - using peptide and aminoacid  
 PT halo:methyl ketone(s).  
 XX PS Claim 1; Col 4; 9pp; English.  
 XX CC The cpds. of the invention inhibit protein phosphorylation. The inventors  
 CC claim a process for inhibiting the growth of tumour cells in a medium  
 CC which comprises contacting the cells with a cpd. of formula (AAFe1654-  
 CC P61661) or a physiologically acceptable salt. (Updated on 03-OCT-2002 to  
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)  
 XX SQ Sequence 4 AA;  
 Query Match 85.7%; Score 18; DB 1; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLL 4  
 RESULT 11  
 AAP71301  
 ID AAP71301 standard; peptide; 4 AA.  
 XX AC AAP71301;  
 XX DT 25-MAR-2003 (revised)  
 DT 15-MAY-1991 (first entry)  
 XX PE Peptide component of cpd. for treating picornavirus infections.  
 DE Picornaviridae; poliovirus; rhinovirus; antiviral agent.  
 KW Synthetic.  
 OS US4636492-A.  
 XX PN 13-JAN-1987.  
 XX PD 29-AUG-1984; 84US-00645426.  
 XX PF 29-AUG-1984; 84US-00645426.  
 XX PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX PA Kettner CA, Korant BD;  
 XX PI WPI; 1987-036897/05.  
 XX DR Treating picorna-virus infection with peptide halo:methyl ketone cpds. -  
 XX PT esp. for treating polio virus and rhino virus infections.  
 XX PS Disclosure; Page 3; 10pp; English.  
 XX CC This peptide is useful as part of a peptide/halo-methyl ketone cpd., for  
 CC treating picornavirus, egpolio- or rhinovirus infections. It inhibits the  
 CC processing of picornavirus capsid proteins by virus encoded proteases.  
 CC See AAP71302-13. See also US4652552. (Updated on 25-MAR-2003 to correct  
 CC PA field.)  
 XX SQ Sequence 4 AA;  
 Query Match 85.7%; Score 18; DB 1; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLL 4  
 RESULT 12  
 AAW41686  
 ID AAW41686 standard; peptide; 4 AA.  
 XX AC AAW41686;  
 XX DT 09-JUN-1998 (first entry)  
 XX DE Tetrapeptide #3.  
 XX KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;  
 KW keratitis; insulin like growth factor-I; IGF-I; eye drop.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "C-terminal amide"  
 XX PN WO9749419-A1.  
 XX PD 31-DEC-1997.  
 XX PF 11-JUN-1997; 97WO-JP002015.  
 XX PR 26-JUN-1996; 96JP-00165612.  
 XX PA (SANT ) SANTEN PHARM CO LTD.  
 XX PI Nishida T, Nakamura M, Nakata K;  
 XX WPI; 1998-076907/07.  
 XX PT Ophthalmic drug composition containing tetra:peptide - is useful as  
 PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,  
 PT dry eye, keratitis.  
 XX PS Disclosure; Page 11; 19pp; Japanese.  
 XX CC This sequence is shown in the specification. The invention relates to an  
 CC ophthalmic drug composition which contains Phe-Gly-Leu-Met-NH2 or its  
 CC medicinally acceptable salts as the active ingredient. It is used,  
 CC together with insulin like growth factor-I (IGF-I), to treat corneal  
 CC disorders such as corneal ulcer, corneal epithelial peeling, dry eye and  
 CC keratitis. The dosage is 0.1-5000 (preferably 1-1000) mg/day of the  
 CC active ingredient and 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The  
 CC preferable form of the composition is eye drops  
 XX SQ Sequence 4 AA;  
 Query Match 85.7%; Score 18; DB 2; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 YGLM 4  
 RESULT 13  
 ABB10092  
 ID ABB10092 standard; peptide; 4 AA.  
 XX AC ABB10092;  
 Query Match 85.7%; Score 18; DB 2; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 YGLM 4  
 RESULT 13  
 ABB10092  
 ID ABB10092 standard; peptide; 4 AA.  
 XX AC ABB10092;

Query Match 85.7%; Score 18; DB 1; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 FGLL 4  
 RESULT 12  
 AAW41686  
 ID AAW41686 standard; peptide; 4 AA.  
 XX AC AAW41686;  
 XX DT 09-JUN-1998 (first entry)  
 XX DE Tetrapeptide #3.  
 XX KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;  
 KW keratitis; insulin like growth factor-I; IGF-I; eye drop.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "C-terminal amide"  
 XX PN WO9749419-A1.  
 XX PD 31-DEC-1997.  
 XX PF 11-JUN-1997; 97WO-JP002015.  
 XX PR 26-JUN-1996; 96JP-00165612.  
 XX PA (SANT ) SANTEN PHARM CO LTD.  
 XX PI Nishida T, Nakamura M, Nakata K;  
 XX WPI; 1998-076907/07.  
 XX PT Ophthalmic drug composition containing tetra:peptide - is useful as  
 PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,  
 PT dry eye, keratitis.  
 XX PS Disclosure; Page 11; 19pp; Japanese.  
 XX CC This sequence is shown in the specification. The invention relates to an  
 CC ophthalmic drug composition which contains Phe-Gly-Leu-Met-NH2 or its  
 CC medicinally acceptable salts as the active ingredient. It is used,  
 CC together with insulin like growth factor-I (IGF-I), to treat corneal  
 CC disorders such as corneal ulcer, corneal epithelial peeling, dry eye and  
 CC keratitis. The dosage is 0.1-5000 (preferably 1-1000) mg/day of the  
 CC active ingredient and 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The  
 CC preferable form of the composition is eye drops  
 XX SQ Sequence 4 AA;  
 Query Match 85.7%; Score 18; DB 2; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FGLM 4  
 DB 1 YGLM 4  
 RESULT 13  
 ABB10092  
 ID ABB10092 standard; peptide; 4 AA.  
 XX AC ABB10092;



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XX DT 26-JUL-2002 (first entry)
XX DE Substance P analog used in wound healing treatment#15.
XX KW Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;
XX KW surgical incision; burn.
XX OS Unidentified.
XX PN WO200213853-A1.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-JP006933.
XX PR 10-AUG-2000; 2000JP-00242489.
XX PR 28-NOV-2000; 2000JP-00361388.
XX PA (SANT ) SANTEN PHARM CO LTD.
XX PA (NISH/) NISHIDA T.
XX PI Nishida T, Nakata K, Nakamura M;
XX WI WI; 2002-269153/31.
XX CC Skin wound healing promoters or skin epidermal extension promoters
XX CC containing substance P analogs and insulin-like growth factor-I for
XX CC treating wounds like tear, abrasion, surgical incision, skin ulcers or
XX CC burns.
XX PS Disclosure; Page 4; 20pp; Japanese.
XX CC The invention relates to skin wound healing promoters, containing
XX CC substance P analogs or their pharmaceutically-acceptable salts, and
XX CC insulin-like growth factor-I as the active ingredient. The promoters are
XX CC for treating wounds like tears, abrasions, surgical incisions, or skin
XX CC ulcers and burns. The current sequence represents a substance P analog
XX CC for use in wound healing treatment
XX SQ Sequence 4 AA;

Query Match 85.7%; Score 18; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
Db :|||
1 YGLM 4

RESULT 14
AAP61707
ID AAP61707 standard; peptide; 4 AA.
AC AAP61707;
XX 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 08-JUN-1991 (first entry)
XX Sequence located immediately adjacent to and upstream of the cleavage
DE site within a virus-specified polypeptide precursor.
DE DE Viral disease; diagnosis; picornavirus.
XX KW Synthetic.
XX OS
XX OS Location/Qualifiers
XX FH
XX FT Misc-difference 1
XX FT /note= "bonede to Boc, Z, Suc, or MeOSuc; Z-carbobenzoxo;
XX FT Bocat-Butyloxycarbonyl; Suc-Succinyl;
XX FT MeOSuc=Methoxysuccinyl"
XX FT

FT Misc-difference 4
FT /note= "Bonded to a chromogenic, fluorogenic,
FT chemiluminescent, radioactive, antigenic, or haptenic
FT indicator group."
XX PN EP187721-A.
XX PD 16-JUL-1986.
XX PF 10-JAN-1986; 86EP-00300147.
XX PR 11-JAN-1985; 85US-00690731.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Kettner CA, Korant BD;
XX WI WI; 1986-184617/29.
XX CC Peptide substrates for virus-specified protease(s) - with C-terminal
XX CC indicator gp. linked by amide or ester linkage.
XX PS Example; p22; 41pp; English.
XX CC The cpds. of the invention are useful in diagnosis of infectious diseases
XX CC caused by viruses which encode a specific protease e.g. picornaviruses.
XX CC (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003
XX CC to correct PA field.)
XX SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3
Db :|||
1 FGL 3

RESULT 15
AAP71312
ID AAP71312 standard; protein; 4 AA.
AC AAP71312;
XX 25-MAR-2003 (revised)
DT 15-MAY-1991 (first entry)
XX Peptide component of cpd. for treating picornavirus infections.
DE DE Picornaviridae; poliovirus; rhinovirus; antiviral agent.
XX KW Synthetic.
XX OS
XX PN US4636492-A.
XX PD 13-JAN-1987.
XX PF 29-AUG-1984; 84US-00645426.
XX PR 29-AUG-1984; 84US-00645426.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Kettner CA, Korant BD;
XX WI WI; 1987-036897/05.
XX CC Treating picorna-virus infection with peptide halo:methyl ketone cpds. -
XX CC esp. for treating polio virus and rhino virus infections.
XX PS Disclosure; Page 4; 10pp; English.

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XX This peptide is useful as part of a peptide/halo-methyl ketone cpd., for  
CC treating picornavirus, egpolio- or rhinovirus infections. It inhibits the  
CC processing of picornavirus capsid proteins by virus encoded proteases.  
CC See AAP71301-11 and AAP71313. See also US4652552. (Updated on 25-MAR-2003  
CC to correct PA field.)

XX  
SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
|||  
Db 1 FGL 3

Search completed: March 23, 2005, 15:12:55  
Job time : 167 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 15:13:04 ; Search time 137 Seconds

(without alignments)  
9.667 Million cell updates/sec

Title: SEQ3

Perfect score: 21

Sequence: 1 fglm 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 9312

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	9	US-09-265-690C-2
2	21	100.0	4	14	US-10-230-133-3
3	21	100.0	4	14	US-10-053-669-2
4	21	100.0	4	16	US-10-695-536-3
5	21	100.0	4	16	US-10-805-881-2
6	21	100.0	4	17	US-10-497-628-2
7	16	76.2	4	9	US-09-879-442A-9
8	16	76.2	4	17	US-10-821-240A-270
9	15	71.4	3	14	US-10-230-133-2
10	15	71.4	3	16	US-10-695-536-2
11	14	66.7	4	9	US-09-879-442A-8
12	14	66.7	4	15	US-10-137-867-328
13	13	61.9	4	9	US-09-879-442A-98

14	13	61.9	4	9	US-09-879-442A-99	Sequence 99, Appl
15	13	61.9	4	9	US-09-943-123-24	Sequence 24, Appl
16	13	61.9	4	14	US-10-087-905-30	Sequence 30, Appl
17	13	61.9	4	14	US-10-087-942-30	Sequence 30, Appl
18	13	61.9	4	14	US-10-087-402-10	Sequence 10, Appl
19	13	61.9	4	14	US-10-083-894-31	Sequence 31, Appl
20	13	61.9	4	14	US-10-196-394-98	Sequence 98, Appl
21	13	61.9	4	14	US-10-202-824-11	Sequence 11, Appl
22	13	61.9	4	15	US-10-359-363A-104	Sequence 104, App
23	13	61.9	4	17	US-10-712-359A-24	Sequence 24, Appl
24	12	57.1	3	14	US-10-121-857-6	Sequence 6, Appl
25	12	57.1	3	14	US-10-255-679-3	Sequence 3, Appl
26	12	57.1	3	14	US-10-208-018-6	Sequence 6, Appl
27	12	57.1	3	14	US-10-104-307-3	Sequence 3, Appl
28	12	57.1	4	8	US-08-484-409-14	Sequence 14, Appl
29	12	57.1	4	8	US-08-484-409-25	Sequence 25, Appl
30	12	57.1	4	9	US-09-804-733A-24	Sequence 24, Appl
31	12	57.1	4	9	US-09-803-126-20	Sequence 20, Appl
32	12	57.1	4	10	US-09-726-470A-29	Sequence 29, Appl
33	12	57.1	4	10	US-09-563-222-1	Sequence 1, Appl
34	12	57.1	4	10	US-09-811-945-15	Sequence 15, Appl
35	12	57.1	4	13	US-10-007-761-62	Sequence 62, Appl
36	12	57.1	4	13	US-10-044-034-1	Sequence 1, Appl
37	12	57.1	4	13	US-10-044-034-25	Sequence 25, Appl
38	12	57.1	4	13	US-10-076-421-3	Sequence 3, Appl
39	12	57.1	4	14	US-10-087-905-14	Sequence 14, Appl
40	12	57.1	4	14	US-10-087-905-17	Sequence 17, Appl
41	12	57.1	4	14	US-10-255-679-2	Sequence 2, Appl
42	12	57.1	4	14	US-10-255-679-5	Sequence 5, Appl
43	12	57.1	4	14	US-10-255-679-11	Sequence 11, Appl
44	12	57.1	4	14	US-10-255-679-12	Sequence 12, Appl
45	12	57.1	4	14	US-10-255-679-13	Sequence 13, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-265-690C-2  
; Sequence 2, Application US/09265690C  
; Publication No. US20010051345A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound M  
; FILE OF INVENTION: for Disease Diagnosis  
; FILE REFERENCE: 1427001  
; CURRENT APPLICATION NUMBER: US/09/265,690C  
; CURRENT FILING DATE: 1999-03-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: AMIDATION  
US-09-265-690C-2

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4

DB 1 FGLM 4

#### RESULT 2

US-10-230-133-3  
; Sequence 3, Application US/10230133  
; Publication No. US20030040625A1

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; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; FILE OF INVENTION: Methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match          100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
DB      1 FGLM 4

RESULT 3
US-10-053-669-2
; Sequence 2, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; FILE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053,669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265,690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-053-669-2

Query Match          100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
DB      1 FGLM 4

RESULT 4
US-10-695-536-3
; Sequence 3, Application US/10695536
; Publication No. US20040110692A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert Clifton
; TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents
; FILE OF INVENTION: And Methods for Treatment of Abnormal Physiological States
; FILE REFERENCE: 800812-0008
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; CURRENT APPLICATION NUMBER: US/10/695,536
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 10/230,133
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-695-536-3

Query Match          100.0%; Score 21; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
DB      1 FGLM 4

RESULT 5
US-10-805-881-2
; Sequence 2, Application US/10805881
; Publication No. US20040171093A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert C.
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound
; FILE OF INVENTION: Magnesium for Disease Diagnosis
; FILE REFERENCE: 800812-0005
; CURRENT APPLICATION NUMBER: US/10/805,881
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 10/053,669
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 10/695,536
; PRIOR FILING DATE: 2003-10-28
; NUMBER OF SEQ ID NOS: 4
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; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-805-881-2

Query Match          100.0%; Score 21; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGLM 4
DB      1 FGLM 4

RESULT 6
US-10-497-628-2
; Sequence 2, Application US/10497628
; Publication No. US20050009752A1
; GENERAL INFORMATION:
; APPLICANT: Teruo Nishida
; APPLICANT: Makoto Inui
; APPLICANT: Masatsugu Nakamura
; TITLE OF INVENTION: NOVEL PEPTIDE AND PHARMACEUTICAL USE OF THE SAME
; FILE REFERENCE: 04355/HG
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; CURRENT APPLICATION NUMBER: US/10/497,628  
; CURRENT FILING DATE: 2004-06-03  
; PRIOR APPLICATION NUMBER: JP 2001-368103  
; PRIOR FILING DATE: 2001-12-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Human  
US-10-497-628-2

Query Match 100.0%; Score 21; DB 17; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGLM 4  
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Db 1 FGLM 4

## RESULT 7

US-09-879-442A-9  
; Sequence 9, Application US/09879442A  
; Patent No. US20020142955A1  
; GENERAL INFORMATION:  
; APPLICANT: CORIXA CORPORATION  
; APPLICANT: Dubois, Vincent  
; APPLICANT: Fernandez, Anne Marie  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Lewis, Evan  
; APPLICANT: Lobl, Thomas J.  
; APPLICANT: Nieder, Matthew H.  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Trouet, Andre  
; APPLICANT: Yarranton, Geoffrey T.  
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS  
; FILE REFERENCE: COUL-015/02US  
; CURRENT APPLICATION NUMBER: US/09/879,442A  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/290,448  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/211,887  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: PCT/US99/30393  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/119,312  
; PRIOR FILING DATE: 1999-02-08  
; PRIOR APPLICATION NUMBER: 60/111,793  
; PRIOR FILING DATE: 1998-12-11  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: Beta-Alanine  
US-09-879-442A-9

Query Match 76.2%; Score 16; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3  
|||  
Db 2 FGL 4

## RESULT 8

US-09-879-442A-9  
; Sequence 9, Application US/09879442A  
; Patent No. US20020142955A1  
; GENERAL INFORMATION:  
; APPLICANT: CORIXA CORPORATION  
; APPLICANT: Dubois, Vincent  
; APPLICANT: Fernandez, Anne Marie  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Lewis, Evan  
; APPLICANT: Lobl, Thomas J.  
; APPLICANT: Nieder, Matthew H.  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Trouet, Andre  
; APPLICANT: Yarranton, Geoffrey T.  
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS  
; FILE REFERENCE: COUL-015/02US  
; CURRENT APPLICATION NUMBER: US/09/879,442A  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/290,448  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/211,887  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: PCT/US99/30393  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/119,312  
; PRIOR FILING DATE: 1999-02-08  
; PRIOR APPLICATION NUMBER: 60/111,793  
; PRIOR FILING DATE: 1998-12-11  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: Beta-Alanine  
US-09-879-442A-9

Query Match 76.2%; Score 16; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3  
|||  
Db 2 FGL 4

## RESULT 8

US-09-879-442A-9  
; Sequence 9, Application US/09879442A  
; Patent No. US20020142955A1  
; GENERAL INFORMATION:  
; APPLICANT: CORIXA CORPORATION  
; APPLICANT: Dubois, Vincent  
; APPLICANT: Fernandez, Anne Marie  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Lewis, Evan  
; APPLICANT: Lobl, Thomas J.  
; APPLICANT: Nieder, Matthew H.  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Trouet, Andre  
; APPLICANT: Yarranton, Geoffrey T.  
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS  
; FILE REFERENCE: COUL-015/02US  
; CURRENT APPLICATION NUMBER: US/09/879,442A  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/290,448  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/211,887  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: PCT/US99/30393  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/119,312  
; PRIOR FILING DATE: 1999-02-08  
; PRIOR APPLICATION NUMBER: 60/111,793  
; PRIOR FILING DATE: 1998-12-11  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: Beta-Alanine  
US-09-879-442A-9

US-10-821-240A-270  
; Sequence 270, Application US/10821240A  
; Publication No. US20050037430A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/821,240A  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: 10/028,075  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 312  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 270  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: metalloproteinase-2  
US-10-821-240A-270

Query Match 76.2%; Score 16; DB 17; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGL 3  
|||  
Db 2 FGL 4

## RESULT 9

US-10-230-133-2  
; Sequence 2, Application US/10230133  
; Publication No. US20030040625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wells, Ibert  
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and  
; TITLE OF INVENTION: methods for treatment of abnormal physiological states  
; FILE REFERENCE: 2892-106  
; CURRENT APPLICATION NUMBER: US/10/230,133  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 09/635,266  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RBS  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: AMIDATION  
US-10-230-133-2

Query Match 71.4%; Score 15; DB 14; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GLM 4  
|||  
Db 1 GLM 3

## RESULT 10

US-10-695-536-2  
; Sequence 2, Application US/10695536  
; Publication No. US20040110692A1  
; GENERAL INFORMATION:

APPLICANT: Wells, Ibert Clifton  
; TITLE OF INVENTION: Antagonists of the Magnesium Binding Defect as Therapeutic Agents  
; FILE REFERENCE: 800812-0008  
; CURRENT APPLICATION NUMBER: US/10/695,536  
; CURRENT FILING DATE: 2003-10-28  
; PRIOR FILING DATE: US 10/230,133  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 09/635,266  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: AMIDATION  
US-10-695-536-2

Query Match 71.4%; Score 15; DB 16; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLM 4  
|||  
Db 1 GLM 3

## RESULT 11

US-09-879-442A-8  
; Sequence 8, Application US/09879442A  
; Patent No. US20020142955A1  
; GENERAL INFORMATION:  
; APPLICANT: CORIXA CORPORATION  
; APPLICANT: Dubois, Vincent  
; APPLICANT: Fernandez, Anne Marie  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Lewis, Evan  
; APPLICANT: Lobl, Thomas J.  
; APPLICANT: Nieder, Matthew H.  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Trouet, Andre  
; APPLICANT: Varranton, Geoffrey T.  
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS  
; FILE REFERENCE: COUL-015/02US  
; CURRENT APPLICATION NUMBER: US/09/879,442A  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/290,448  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/211,887  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: PCT/US99/30393  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 60/119,312  
; PRIOR FILING DATE: 1999-02-08  
; PRIOR APPLICATION NUMBER: 60/111,793  
; PRIOR FILING DATE: 1998-12-11  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: Beta-Alanine  
US-09-879-442A-8

Query Match 66.7%; Score 14; DB 9; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
|||  
Db 2 FGL 4

## RESULT 12

US-10-137-867-328  
; Sequence 328, Application US/10137867  
; Publication No. US20030207349A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C146  
; CURRENT APPLICATION NUMBER: US/10/137,867  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 328  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-867-328

Query Match 66.7%; Score 14; DB 15; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
|||  
Db 2 FGL 4

## RESULT 13

US-09-879-442A-98  
; Sequence 98, Application US/09879442A  
; Patent No. US20020142955A1  
; GENERAL INFORMATION:  
; APPLICANT: CORIXA CORPORATION  
; APPLICANT: Dubois, Vincent  
; APPLICANT: Fernandez, Anne Marie  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Lewis, Evan  
; APPLICANT: Lobl, Thomas J.  
; APPLICANT: Nieder, Matthew H.  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Trouet, Andre  
; APPLICANT: Varranton, Geoffrey T.  
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS  
; FILE REFERENCE: COUL-015/02US  
; CURRENT APPLICATION NUMBER: US/09/879,442A  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 60/290,448

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; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/211,887
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US99/30393
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/119,312
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 60/111,793
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: 2-Thienylalanine
; US-09-879-442A-98

Query Match          61.9%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGL 3
        :||
Db      2 YGL 4

RESULT 14
US-09-879-442A-99
; Sequence 99, Application US/09879442A
; Patent No. US20020142955A1
; GENERAL INFORMATION:
; APPLICANT: CORIXA CORPORATION
; APPLICANT: Dubois, Vincent
; APPLICANT: Fernandez, Anne Marie
; APPLICANT: Gangwar, Sanjeev
; APPLICANT: Lewis, Evan
; APPLICANT: Lobl, Thomas J.
; APPLICANT: Nieder, Matthew H.
; APPLICANT: Pickford, Lesley B.
; APPLICANT: Trouet, Andre
; APPLICANT: Varranton, Geoffrey T.
; TITLE OF INVENTION: ENZYME CLEAVABLE PRODRUG COMPOUNDS
; FILE REFERENCE: COUL-015/02US
; CURRENT APPLICATION NUMBER: US/09/879,442A
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/290,448
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/211,887
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US99/30393
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/119,312
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 60/111,793
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Beta-Alanine
; US-09-879-442A-99

Query Match          61.9%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FGL 3
        :||
Db      2 YGL 4

RESULT 15
US-09-943-123-24
; Sequence 24, Application US/09943123
; Publication No. US20020192701A1
; GENERAL INFORMATION:
; APPLICANT: CHANG, Y-H
; APPLICANT: MITCKA, W.S.
; TITLE OF INVENTION: Dominant Negative Variants of Methionine Aminopeptidase
; FILE REFERENCE: 16153-8007
; CURRENT APPLICATION NUMBER: US/09/943,123
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-09-943-123-24

Query Match          61.9%; Score 13; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GLM 4
        :||
Db      2 GMM 4

Search completed: March 23, 2005, 15:25:39
Job time : 138 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 23, 2005, 15:04:03 ; Search time 41 Seconds  
(without alignments)  
7.283 Million cell updates/sec

Title: SEQ3

Perfect score: 21

Sequence: 1 fglm 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 12390

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	1	US-08-441-591-63
2	21	100.0	4	1	US-08-303-362A-63
3	21	100.0	4	3	US-09-265-690C-2
4	21	100.0	4	4	US-09-635-266-3
5	21	100.0	4	4	US-10-230-133-3
6	21	100.0	4	5	PCT-US95-05600-80
7	16	76.2	4	2	US-08-747-137-124
8	16	76.2	4	3	US-08-722-128A-20
9	15	71.4	3	4	US-09-635-266-2
10	15	71.4	3	4	US-10-230-133-2
11	15	71.4	4	2	US-08-070-301-8
12	15	71.4	4	2	US-08-433-401-4
13	14	66.7	4	3	US-08-793-701-25
14	14	66.7	4	4	US-09-579-264-25
15	13	61.9	4	2	US-08-429-964-37
16	13	61.9	4	3	US-08-812-586-60
17	13	61.9	4	4	US-08-669-656A-11
18	13	61.9	4	4	US-09-535-832A-56
19	13	61.9	4	4	US-09-665-362A-31
20	13	61.9	4	4	US-09-665-637-31
21	13	61.9	4	4	US-10-087-402-10
22	13	61.9	4	5	PCT-US93-08062-37
23	12	57.1	3	1	US-08-343-943-4
24	12	57.1	3	2	US-09-060-455-2
25	12	57.1	3	4	US-09-150-621-3
26	12	57.1	3	4	US-10-121-857-6
27	12	57.1	4	1	US-07-657-769B-58

28 12 57.1 4 1 US-07-822-924-3 Sequence 3, Appli  
29 12 57.1 4 1 US-07-822-924-5 Sequence 5, Appli  
30 12 57.1 4 1 US-07-822-924-7 Sequence 7, Appli  
31 12 57.1 4 1 US-08-285-777-1 Sequence 1, Appli  
32 12 57.1 4 1 US-08-147-270A-1 Sequence 1, Appli  
33 12 57.1 4 1 US-07-969-307A-1 Sequence 1, Appli  
34 12 57.1 4 1 US-07-969-307A-2 Sequence 2, Appli  
35 12 57.1 4 1 US-07-969-307A-3 Sequence 3, Appli  
36 12 57.1 4 1 US-08-127-904-11 Sequence 11, Appli  
37 12 57.1 4 1 US-08-431-539-4 Sequence 4, Appli  
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39 12 57.1 4 1 US-08-429-732-20 Sequence 20, Appli  
40 12 57.1 4 1 US-07-789-184-108 Sequence 108, App  
41 12 57.1 4 1 US-08-549-008-10 Sequence 10, Appli  
42 12 57.1 4 1 US-08-624-123-11 Sequence 11, Appli  
43 12 57.1 4 1 US-08-077-252B-20 Sequence 20, Appli  
44 12 57.1 4 1 US-08-475-263-108 Sequence 108, App  
45 12 57.1 4 1 US-08-485-886-108 Sequence 108, App

#### ALIGNMENTS

RESULT 1  
US-08-441-591-63  
; Sequence 63, Application US/08441591  
; Patent No. 5637682  
; GENERAL INFORMATION:  
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.  
; TITLE OF INVENTION: HIGH-AFFINITY  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS  
; TITLE OF INVENTION: TO THE TACHYKININ  
; TITLE OF INVENTION: SUBSTANCE P  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,591  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/303,362  
; FILING DATE: 9-SEPTEMBER-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/931,473  
; FILING DATE: 17-AUGUST-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/117,991  
; FILING DATE: 8-SEPTEMBER 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/964,624  
; FILING DATE: 21-OCTOBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX21/C  
; TELECOMMUNICATION INFORMATION:

```
/ TELEPHONE: (303) 793-3333
/ TELEFAX: (303) 793-3433
/ INFORMATION FOR SEQ ID NO: 63:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-441-591-63

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4

RESULT 2
US-08-303-362A-63
; Sequence 63, Application US/08303362A
; Patent No. 5648214
; GENERAL INFORMATION:
; APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,362A
; FILING DATE: 9-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS: single
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/ TOPOLOGY: linear
US-08-303-362A-63

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4

RESULT 3
US-09-265-690C-2
; Sequence 2, Application US/09265690C
; Patent No. 6372440
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
; TITLE OF INVENTION: for Disease Diagnosis
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-2

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4

RESULT 4
US-09-635-266-3
; Sequence 3, Application US/09635266
; Patent No. 6455734
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: N1427-002
; CURRENT APPLICATION NUMBER: US/09/635,266
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-09-635-266-3

Query Match 100.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 1 FGLM 4
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Met-Amide"
US-08-747-137-124

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Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FGL 3
   |||
DB 1 FGL 3

```

```

RESULT 8
US-08-722-126A-20
; Sequence 20, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-20

```

```

Query Match 76.2%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FGL 3
   |||
DB 2 FGL 4

```

```

RESULT 9
US-09-635-266-2
; Sequence 2, Application US/09635266
; Patent No. 6455734
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: N1427-002
; CURRENT APPLICATION NUMBER: US/09/635,266
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: AMIDATION
US-09-635-266-2

```

```

Query Match 71.4%; Score 15; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 GLM 4
   |||
DB 1 GLM 3

```

```

RESULT 10
US-10-230-133-2
; Sequence 2, Application US/10230133
; Patent No. 6664420
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; TITLE OF INVENTION: methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09

```

NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: AMIDATION  
US-10-230-133-2

Query Match 71.4%; Score 15; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLM 4  
|||  
Db 1 GLM 3

## RESULT 11

US-08-070-301-8  
; Sequence 8, Application US/08070301  
; Patent No. 5871995

## ; GENERAL INFORMATION:

; APPLICANT: IIDA, Toshio  
; APPLICANT: KAMINUMA, Toshihiko  
; APPLICANT: FUSE, Yuka  
; APPLICANT: TAJIMA, Masahiro  
; APPLICANT: YANAGI, Mitsuo  
; APPLICANT: OKAMOTO, Hiroshi  
; APPLICANT: KISHIMOTO, Jiro  
; APPLICANT: IFUKU, Ohji  
; APPLICANT: KATO, Ichiro

; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL  
; TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wegner, Cantox, Mueller & Player, P.C.  
; STREET: 1233 20th Street, N.W.  
; CITY: Washington

; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036-8218

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/070,301  
; FILING DATE: 24-MAY-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 1-209687

; FILING DATE: 15-AUG-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 1-181933

; FILING DATE: 31-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-76331

; FILING DATE: 26-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-106412

; FILING DATE: 24-APR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-205475

; FILING DATE: 02-AUG-1990

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: P-450-22830

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-040

; TELEFAX: (202) 835-0605

; TELEX: 440706

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; OTHER INFORMATION: peptide

US-08-070-301-8

Query Match 71.4%; Score 15; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLM 4  
|||  
Db 1 GLM 3

## RESULT 12

US-08-433-401-4

; Sequence 4, Application US/08433401

; Patent No. 5872097

## ; GENERAL INFORMATION:

; APPLICANT: Ph lenhag, Karin I.

; APPLICANT: Fryklund, Linda

; APPLICANT: Larsson, Bo C.

; APPLICANT: Nyberg, Fred J.

; APPLICANT: Westin-SJ dahl, Gertrud E.

; APPLICANT: Ludin, Ronny

; TITLE OF INVENTION: New Oligopeptides with Affinity to

; TITLE OF INVENTION: Opioid Receptors

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pollock, Vande Sande & Priddy

; STREET: 1990 M Street, N.W., Suite 800

; CITY: Washington

; STATE: D.C.

; COUNTRY: US

; ZIP: 20036-0088

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,401

; FILING DATE: 18-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/SE93/00986

; FILING DATE: 18-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9203496-6

; FILING DATE: 20-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Amernick, Burton A.

; REGISTRATION NUMBER: 24,852

; REFERENCE/DOCKET NUMBER: 151/00118

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 331-7111

; TELEFAX: (202) 223-2596

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-433-401-4

Query Match 71.4%; Score 15; DB 2; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4  
 :||:  
 Db 1 YGLL 4

RESULT 13  
 US-08-793-701-25  
 ; Sequence 25, Application US/08793701  
 ; Patent No. 6248581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GICQUEL, Brigitte  
 ; APPLICANT: LIM, Eng Mong  
 ; APPLICANT: PORTNOI, Denis  
 ; APPLICANT: BERTHET, Francois-Xavier  
 ; APPLICANT: TIMM, Juliano  
 ; TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
 ; NUMBER OF SEQUENCES: 63  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: c/o FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
 ; ADDRESSEE: DUNNER, L.L.P.  
 ; STREET: 1300 I Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/793,701  
 ; FILING DATE: 09-JUN-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/FR9501133  
 ; FILING DATE: 30-AUG-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 94/10585  
 ; FILING DATE: 02-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McDonnell, Leslie A.  
 ; REGISTRATION NUMBER: 34,872  
 ; REFERENCE/DOCKET NUMBER: 02356.0075  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 408-4132  
 ; TELEFAX: (202) 408-4400  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-793-701-25

Query Match 66.7%; Score 14; DB 3; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
 :||:  
 Db 2 FGI 4

RESULT 14  
 US-09-579-264-25  
 ; Sequence 25, Application US/09579264

Patent No. 6565855  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GICQUEL, Brigitte  
 ; APPLICANT: LIM, Eng Mong  
 ; APPLICANT: PORTNOI, Denis  
 ; APPLICANT: BERTHET, Francois-Xavier  
 ; APPLICANT: TIMM, Juliano  
 ; TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
 ; NUMBER OF SEQUENCES: 63  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: c/o FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
 ; ADDRESSEE: DUNNER, L.L.P.  
 ; STREET: 1300 I Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/579,264  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/793,701  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 94/10585  
 ; FILING DATE: 02-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McDonnell, Leslie A.  
 ; REGISTRATION NUMBER: 34,872  
 ; REFERENCE/DOCKET NUMBER: 02356.0075  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 408-4132  
 ; TELEFAX: (202) 408-4400  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-579-264-25

Query Match 66.7%; Score 14; DB 4; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGL 3  
 :||:  
 Db 2 FGI 4

RESULT 15  
 US-08-429-964-37  
 ; Sequence 37, Application US/08429964  
 ; Patent No. 5962243  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BROWN, MICHAEL S.  
 ; APPLICANT: GOLDSTEIN, JOSEPH L.  
 ; APPLICANT: REISS, YUVAL  
 ; APPLICANT: JAMES, GUY L.  
 ; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
 ; NUMBER OF SEQUENCES: 85  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ARNOLD, WHITE & DURKEE  
 ; STREET: P.O. BOX 4433  
 ; CITY: HOUSTON

STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/429,964  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,625  
FILING DATE: 16-FEB-1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/822,011  
FILING DATE: ABANDONED  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US/91/02650  
FILING DATE: 18-APR-1991  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/615,715  
FILING DATE: 20-NOV-1990  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/510,706  
FILING DATE: 18-APR-1990 (ABANDONED)  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PARKER, DAVID L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:432/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-429-964-37

Query Match 61.9%; Score 13; DB 2; Length 4;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GLM 4  
Db 2 GIM 4

Search completed: March 23, 2005, 15:14:28  
Job time : 42 secs

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

Application Number



10/305,418

Application/Control No.

Applicant(s)/Patent under  
Reexamination

BOHLMANN ET AL.

Examiner

Art Unit

Barbara P. Badio, Ph.D.

1617